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GenCore version 5.1.6
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OM protein - protein search, using sw model

5, 2004, 10:24:46; Search time 21 Seconds (without alignments) 59:547 Million cell updates/sec September Run on:

US-09-761-636A-5 Title: Perfect score:

1 CASELGKSTNTFC 13 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues Searched:

1827 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 13

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*

pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	The section of the se	antigen v	l antigen re		1 receptor	l receptor	l antigen r	l receptor b	l antigen r	lantigen	receptor	antigen ,	antigen	antigen		receptor	receptor	receptor	-cell receptor	chain V-D-J	cell receptor b	-cell receptor b	-cell recentor	-cell antiden v	-cell recentor	COLT TOCOPTOR	-Cell antigen v	Cell mecentor	-cell antigen r
SUMMARIES	ΩI	PT0216	S47394	S47357	2654	PH1463	PH1466	S47400	PT0217	S47391	847383	S57575	S47395	847381	S47382	S23371	PH0947	PH1469	PH0931	PH1457	PH1583	10	S26559	S26554	847363	PH1467	46	847390	114	37
	DB	7	7	7	7	7	7	7	(1	7	7	N	7	~	7	7	7	~	~	7	7	7	7	7	7	7	7	7	7	N
	Query Match Length	12	12	13	12	12	12	13	11	12	13	11	12	13	13	10	11	12	12	12	11	12	12	12	12	12	12	13	12	13
dю	Query Match	ė.	•	ä	40.3	æ.	œ.	œ.	7.	۲.	7.	ġ	9	6.	5.	34.7	4	4	34.7	4	S.	m	3	m	3	3	3	3	3	N
	Score	33.5	30	29.5	29	28	28	28	27	27	27	56	56	26	25.5	25	25	25	N	24.5	24	24	24	24	24	24	24	24	23.5	۳.
	Result No.	н	0	m	4	D.	9	7	œ ·	ወ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

ò q RESULT 3 S47357

T-cell receptor be	T-cell receptor be	receptor	receptor	receptor	receptor		T-cell recentor be			T-Cell antigen rec				receptor	
\$26557	\$2655.6	826553	PH1462	PH1470	PH1464	A23695	\$26541	PH1458	847356	847378	S47385	PH0927	\$26546	S26547	826555
0	N	N	~	7	7	N	N	7	7	N	~	~	N	~	7
12	12	12	12	12	12	13	12	12	13	13	13	10	12	12	12
31.9	31.9	31.9	31.9	31.9	31.9	31.9	31.2	31.2	31.2	31.2	31.2	30.6	30.6	30.6	30.6
23	23	23	23	23	23	23	22.5	22.5	22.5	22.5	22.5	22	22	22	22
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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T-cell receptor beta chain V-J region (4-1-G.4) - mouse (fragment)
C.Species: Mus musculus (house mouse)
C.Species: May-1997
C.Species: May-1997
C.Species: Musculus (house mouse)
C.Species: Musculus (house)
C.Species: Musculus (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T-cell antigen receptor VJ junction beta chain - human C.Species: Homo sapiens (man) C.Date: 13-341-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999 C.Accession: S47394; S47369 S.Lehner, P.J. submitted to the EMBL Data Library, August 1994 A.Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T C A.Reference number: S47355 A.Reference number: S47354 A.Reference number: S47394 A.Reference number: S47394 A.Residues: preliminary A.Rolcule type: mRNA A.Residues: 1-12 c.LEH A.Residues: 1-12 c.LEH A.Residues: 1-12 c.LEH A.Residues: 1-12 c.LEH A.Residues: T-cell receptor
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50.0%; Pred. No. 51;
Live 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 72.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CASELGKSTNT 11
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Matches
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S47394
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T-call receptor beta chain (clone A3/74.1) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 11-Apr-1995
C;Accession: PH1466
R;Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; Ko J. Exp. Med. 177; 81-820, 193
J; Exp. Med. 177; 81-820, 193
J;Title: T cell receptor selection by and recognition of two class I major histocompatib A;Reference number: PH1430; MUID:93171821; PMID:8436911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T-cell receptor beta chain V-J region (4-1-E.2) - mouse (fragment)
T-cell receptor beta chain V-J region (4-1-E.2) - mouse (fragment)
T-cell receptor beta chain (house mouse)
C;Species: Musculus (house mouse)
C;Accession: PT0217
C;Accession: PT0217
R;Nakano, N.; Kikutani, H.; Nishimoto, H.; Kishimoto, T.
R;Nakano, N.; Kikutani, H.; Nishimoto, H.; Kishimoto, T.
A;Nakano, N.; Kikutani, H.; Nishimoto, H.; Kishimoto, H.; Kishimoto, T.
A;Nakano, N.; Kikutani, H.; Nishimoto, H.; Kishimoto, H.; Kishimoto, T.
A;Nakano, N.; Kikutani, H.; Nishimoto, H.; Kishimoto, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
R;Lehner, P.J.
submitted to the EMBL Data Library, August 1994
A;Description: Human H.A-A0201 restricted recognition of influenza A is dominated by T (A)Accession: 847400
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:Z35678; NID:g527535; PIDN:CAA84747.1; PID:g527536
C;Keywords: T-cell receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                 Gaps
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Pred. No. 1.3e+02;
2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 28; DB 2; Length 12;
Pred. No. 1.2e+02;
1; Mismatches 1; Indels
Score 28; DB 2; Length 12; Pred. No. 1.2e+02;
                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T-cell antigen receptor VJ junction beta chain - human
                                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Experimental source: cytolytic T-lymphocyte C; Superfamily: immunoglobulin homology C; Keywords: receptor; T-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 38.9%;
Best Local Similarity 71.4%;
Matches 5; Conservative
      38.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                    5; Conservative
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Best Local Similarity
Matches 5; Conserva
                                                                                                                                                                      ||| || :
CASSLGNT 8
                                                                                                                               1 CASELGKS 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CASELGK 7
         Query Match
Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Regidues: 1-12 < CAS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: mRNA
A;Residues: 1-13 <LEH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: PH1466
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C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C;Accession: S47357
R;Lehner, P.J.
submitted to the EMBL Data Library, August 1994
A;Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T of A;Accession: S47355
A;Accession: S47357
A;Accession: S47357
A;Accession: January
A;Wolecule type: mRNA
A;Residues: 1-13 <LEB>
A;Csoss-references: EMBL: Z35681; NID:g527451; PIDN:CAA84750.1; PID:g527452
C;Keywords: T-cell receptor
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C,Superfamily: immunoglobulin V region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 12;
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A;Residues: 1-12 <CAS>
A;Cross-references: EMBL:X67999
A;Experimental source: cytolytic T-lymphocyte, clone Cw3/A8
                T-cell antigen receptor VJ junction beta chain - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 29; DB 2;
Pred. No. 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 29.5; DB Pred. No. 68; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Molecule type: mRNA
A,Residues: 1-12 <CAS>
A,Experimental source: cytolytic T-lymphocyte
C,Superfamily: immunoglobulin homology
C,Keywords: receptor; T-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 63.6%;
Matches 7; Conservative 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 40.3%;
Best Local Similarity 62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references: EMBL: X68000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Conservative
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1 CASS-GRSTDT 10
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1 CASSLGET 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA A; Residues: 1-12 < CA2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Accession: S26550
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Matches

RESULT 5

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Gaps

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C. Species: Home sapiens (wa) Junction Deta chain - human C. Species: Home sapiens (man) - human C. Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999 C. Accession: S47381
R. Jehner, P. J.
A. Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T C A; Accession: S47381
A; Accession: S47381
A; Accession: S47381
A; Accession: Jethinary
A; Accession: Jethinary
A; Accession: Jethinary
A; Residues: 1-13 < LEH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  First P.J.
Submitted to the EMBL Data Library, August 1994
Submitted to the EMBL Data Library, August 1994
A;Description: Human HiA-A0201 restricted recognition of influenza A is dominated by A;Reference number: 847355
A;Accession: 847395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T-cell antigen receptor VJ junction beta chain - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C;Accession: S47395
                                                  A,Accession: S57575
A,Status: preliminary
A,Molecule type: mRNA
A,Residues: 1-11 <BUR>
A;Residues: 1-11 <BUR>
A;Cross-references: EMBL:Z49953; NID:g887510; PIDN:CAA90224.1; PID:g887511
C;Keywords: T-cell receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-12 <LEH>
A;Cross-references: EMBL:Z33715; NID:g527525; PIDN:CAA84784.1; PID:g527526
C;Keywords: T-cell receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Cross-references: EMBL:Z35698; NID:g527487; PIDN:CAA84767.1; PID:g527488
C,Keywords: T-cell receptor
                                                                                                                                                                                                                                                                                       Score 26; DB 2; Length 11;
Pred. No. 2.5e+02;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 26; DB 2; Length 12;
Pred. No. 2.7e+02;
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41.7%; Pred. No. 2.9e+02;
Live 1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             847381
T-cell antigen receptor VJ junction beta chain - human
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T-cell antigen receptor VJ junction beta chain - human
C;Species: Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                           36.18;
71.48;
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50.0%;
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Best Local Similarity 71.4
Matches 5: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CASELGKSTNTF 12
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                              A; Reference number: S57494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 6; Conserva
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Best Local Similarity
Local 5; Conserve
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1 CASQGGK 7
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C;Species: Homo sapiens (man)
C;Date: 19-0ct-1995 #sequence_revision 17-Nov-1995 #text_change 05-Nov-1999
C;Accession: S57575
R;Burrows, S.R.; Silins, S.L.; Moss, D.J.; Khanna, R.; Misko, I.S.; Argaet, V.P.
Submitted to the EMBL Data Library, June 1995
A;Description: T cell receptor repertoire for a viral epitope in humans is diversified b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Molecule type: mRNÁ
A,Residues: 1-12 <LEH>
A,Cross-references: EMBL:235712; NID:9527519; PIDN:CAA84781.1; PID:9527520; EMBL:235701;
C;Keywords: T-cell receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C;Accession: 847391; 847386
R;Lehner, P.J.
submitted to the EMBL Data Library, August 1994
A;Description: Human HiA-A0201 restricted recognition of influenza A is dominated by T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T-cell antigen receptor VJ junction beta chain - human Cispecies: Homo sapiens (man) Cispecies: Homo sapiens (man) Cispecies: Homo sapiens (man) Cispecies: Homo sapiens (man) Cistersion: 347383 Richner, P.J. Richner, S.J. Rich
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A;Molecule type: mRNA
A;Residues: 1-13 <LEH>
A;Cross-references: EMBL:Z35709; NID:g527513; PIDN:CAA84778.1; PID:g527514
C;Keywords: T-cell receptor
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                                                                                                     Score 27; DB 2; Length 11;
Pred. No. 1.6e+02;
0; Mismatches 1; Indels
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847391
T-cell antigen receptor VJ junction beta chain - human
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Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                        37.5%;
83.3%;
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50.0%;
                                                                                           Query Match
Best Local Similarity 83.3
Matches 5; Conservative
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A;Residues: 1-11 <NAK>
C;Keywords: T-cell receptor
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A;Accession: 847391
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Best Local Similarity
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1 CASSMGGS
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Tacall receptor alpha chain J region - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
By: Pluschke, G:; Ricken, G:; Taube, H.; Kroninger, S:; Melchers, I:; Peter, H.H.; Eichman Eur. J. Immunol. 21, 2749-2754, 1991
A;Pluschke, G:; Ricken, G:; 
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999 C;Accession: S47382; S47370 B:Lehner, P.J.
R:Lehner, P.J.
B:Lehner, P.J.
B:Lehne
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Best Local Similarity 54.5%; Pred. No. 3.6e+02;
Matches 6; Conservative 3; Mismatches 1;
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Job time : 21 secs
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Best Local Similarity
Matches 5; Conserv
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2 SGEAGKST
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campylobact macrobrachi

bacillus su polyodon sp vespa manda

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bos taurus

score:

Title: Perfect :

Sequence:

protein

Run on:

Scoring table:

Searched:

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TISSUE=Protonema;

X MEDLINE=97275459; PubMed=9129336;

X Kasten B., Buck F., Nuske J., Reski R.;

K Kasten B., Buck F., Nuske J., Reski R.;

XT Dlastid enzymes.";

Planta 201261-27(1997).

Y plastid enzymes.";

L Planta 201261-27(1997).

C -! FUNCTION: May be involved in the regulation of photosystem II.

C -! FUNCTION: May be involved in the regulation of photosystem II.

C -! FUNCTION: By light.

C -! SIMILARITY: Belongs to the psbp family.

XM Photosynthesis; Photosystem II; Chloroplast; Thylakoid; Membrane;

KW Multigene family.

FT NOW TER.

SQÜENCE 12 AA; 1182 MW; 8D2B0D54D7C44DC5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 44, Last sequence update)
16-0CT-2001 (Rel. 44, Last annotation update)
0xygen-evolving enhancer protein 2 (OEB) (24 kDa subunit of oxygen evolving system of photosystem II) (Fragment).
Physocomitralla patens (Moss).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Punaridae; Runariales; Punariaceae; Physcomitrella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
23 kba structural polyprotein (Fragment).
White spot syndrome virus (WSSV).
Viruses; dsDNA viruses, no RNA stage; Nimaviridae; Whispovirus.
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4; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                12 AA.
                                                                                                                                                                                                                                                                                                                               ALIGNMENTS
FARB MACRS
LPKZ_LOCMI
SYK_CAMUP
SYKL4_LOCMI
TKL4_LOCMI
TKNB_CHICK
TYNB_ONCMY
TKNC_RANCA
TKNC_RANCA
URAG_HUMAN
URGG_BACSU
UR2_POLSP
                                                                                                                                                                                                                                CRBL VESMA
ITB5 BOVIN
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MEDLINE=20214217; PubMed=10752552;
Wang Q., Poulos B.T., Lightner D.V.;
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P80431
            GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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LIGA_TRAVE
COMP_RAT
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FARB_ASCSU
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"Protein analysis of geographic isolates of shrimp white spot syndrome
                                                                                                                                                                                                                                                                                                     -!- PATHWAY: Lignin degradation, first step.
-!- SIMILARITY: Belongs to the peroxidase family. Ligninase subfamily.
PIR; S04013; S04013.
InterPro, IPR002016; Peroxidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUL-1999 (Rel. 38, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Oxygen-evolving enhancer protein 2 (OEE2) (23 kDa subunit of oxygen
evolving system of photosystem II) (Fragment).
                                                                                                                                                                                                                                  Trametes versicolor (White-rot fungus).
Eukaryota, Fungi, Basidiomycota; Hymenomycetes; Homobasidiomycetes;
Aphyllophorales; Trametes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Prbus pinaster (Maritime pine).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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01-FEB-1991 (Rel. 17, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ligninase A (EC 1.11.1.14) (Diarylpropane peroxidase) (Lignin
                                                                Score 20; DB 1; Length 12;
Pred. No. 1.2e+03;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00435; PEROXIDASE 1; PARTIAL.
PROSITE; PS00436; PEROXIDASE 2; PARTIAL.
Oxidoreductase; Peroxidase; Iron; Heme; Glycoprotein;
Multigene family; Lignin degradation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13 AA; 1298 MW; 22C50ED5872A4338 CRC64;
                                            12 AA; 1323 MW; 0C0F41E91D51A724 CRC64;
          virus.";
Arch. Virol. 145:263-274(2000).
-!- FUNCTION: STRUCTURAL COMPONENT OF THE VIRION.
NON_TER
12
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                                                                                                                                                                                                                                                                                                 MEDLINE=89211432; PubMed=2707445;
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                                                                27.8%;
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                                                                            Local Similarity 57.1 tes 4; Conservative
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                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                 (Fragment)
                                                                                                       4 ELGKSTN 10
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Matches 4; Conserv
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                                                                                                                         EFGNLTN
                                                                                                                                                                                                                                                                      NCBI_TaxID=5325;
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P81668;
                                                                                                                                                                                                                                peroxidase)
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P200<u>1</u>1;
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mitochondrial electron transport.

-!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + 0(2) = 4 ferricytochrome c + 2 H(2)0.
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MEDLINE=95324529; PubMed=7601105;
Schaegger H., Noack H., Halangk W., Brandt U., von Jagow G.;
Schaegger H., Noack H., Halangk W., Brandt U., von Jagow G.;
Cytochrome-c oxidase in developing rat heart. Enzymic properties and amino-terminal sequences suggest identity of the fetal heart and the adult liver isoform...;
Eur. J. Biochem. 230:235-241(1995).
Eur. J. Biochem. 230:235-241(1995).
- I- FUNCTION: This protein is one of the nuclear-coded polypeptide chains of cytochrome c oxidase, the terminal oxidase in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      kattus norvegicus (kat).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                               proteins...

Proteins...

Electrophoresis 20:1098-1108(1999).

Electrophoresis 20:1098-1108(1999).

Electrophoresis 20:1098-1108(1999).

-:- SUBCELLUIAR DOCATION: Chloroplast thylakoid membrane; associated with the photosystem II complex (By similarity).

-:- MISCELLANBOUS: On the 2D-gel the determined pl of this protein (Spot NIT9) is: 5.9, its MW is: 2.2 kDa..

-:- SIMILARITY: Belongs to the psbb family.

-:- SIMILARITY: Belongs to the psbb family.

Photosynthesis; Photosystem II; Chloroplast; Thylakoid; Membrane.

NON TER 13
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                                                                                                                                                                                       MEDLINE-99274088; PubMed-10344291;
Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
Frigerio J.-M., Plomion C.;
"Separation and characterization of needle and xylem maritime pine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FBB-2003 (Rel. 41, Last amortation update)
Cytochrome c oxidase polypeptide VIIb, mitochondrial (EC 1.9.3.1)
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Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
VCBL_TaxID=71647;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26.4%; Score 19; DB 1; Length 10; 66.7%; Pred. No. 1.5e+03; Live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27.8%; Score 20; DB 1; Length 13; 42.9%; Pred. No. 1.2e+03; tive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 AA; 1210 MW; CFC70EB771A33326 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; S65387; S65387.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 GKSTNTF 12
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us-09-761-636a-5.closed.rsp

UR2B CATCO

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SEQUENCE.
MEDLINE=88326335; PubMed=3415697;
Pawar H.S., Kannan K., Srinivasan M.C., Vartak H.G.;
"Purification and characterisation of glucose (xylose) isomerase from
                                                                                                                                 Cyprinus carpio (Common carp).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinus.

NCBI_TaxID=7962;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chainia sp. (NCL 82-5-1)...
Biochem. Biophys. Res. Commun. 155:411-417(1988).
-!- FUNCTION: Involved in D-xylose catabolism.
-!- CATALYTIC ACTUALYTYTY: D-xylose = D-xylulose.
-!- COFACTOR: Binds 2 magnesium ions per subunit (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23.6%; Score 17; DB 1; Length 12; 75.0%; Pred. No. 4.18+03; cive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to the xylose isomerase family.
PIR; A31576; A31576.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          G -> S.
73960A9FB879CEBB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptomycineae; Streptomycetaceae; Streptomyces NCBI_TaxID=1931;
                                                            104561;
13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Urotensin II-beta (UII-beta) (U-II-beta)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HAMAP, MF 00455; -; 1.
InterPro; IPR001998; Xylose isom.
PROSITE; PS00172; XYLOSE_ISOMERASE_1; PARTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Xylose isomerase (EC 5.3.1.5) (Fragment).
                                                    12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptomyces sp. (strain NCL 82-5-1)
                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001483; Urotensin II. Pfam; PF02083; Urotensin II; 1. PROSITE; PS00984; UROTENSIN II; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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2 2
12 AA; 1407 MW;
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                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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P19149;
01-NOV-1990 (
                                                   CYPCA
                                                                                                                                                                                                                                 SEQUENCE.
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                                   UR2B CYPCA
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Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Catostomidae; Catostomus.
                                                                                                                                                                                                       McMaster D., Lederis K.; "Isolation and amino acid sequence of two urotensin II peptides from Catostomus commersoni urophyses.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
Ascarididae; Ascaris.
NCBI_TaxID=6253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cowden C., Stretton A.O.W.;
"Eight novel FWRFamide-like neuropeptides isolated from the nematode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ascaris suum.";
Peptides 16:491-500(1995).
-!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
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Pred. No. 2.9e+03;
2; Mismatches 4; Indels
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12 AA; 1437 MW; 73961BDBBB79CEBB CRC64;
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9CAEC650D6886B05 CRC64;
                        13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Catostomus commersoni (White sucker).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
   12 AA
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                                                                                                                                                                                          MEDLINE=84041959; PubMed=6138758;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25.0%;
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                                                                                                                                                                                                                                                     Peptides 4:367-373(1983)
 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Conservative
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MOD_RES 13 13
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Matches 3; Conserv
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Best Local Similarity
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                                                                                                                                                NCBI_TaxID=7971;
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CATCO
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P43173;
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SEQUENCE
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P28878;
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SEQUENCE
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ID TA10 1
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MEDLINE=95075727; PubMed=7984492;

A Lundquist C.T., Clottens F.L., Holman G.M., Nichols R., Nachman R.J.,

A Naeseal D.R.;

T callitachykinin I and II, two novel myotropic peptides isolated from

T tachykinins.";

Peptides 15:761-768(1994).

I. Peptides 15:761-768(1994).

I. FUNCTION: Myoactive pected.

-! FUNCTION: Myoactive pected.

-! STMILARITY: SOME SIMILARITY TO TACHYKININS.

TTACHYKININ: Neuropeptide; Amidation.

THOM RES.

THOM RES.

THE AMIDATION.

SEQÜENCE 11 AA; 1103 MW; 15D7E3F9C9CDD444 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Calliphora vomitoria (Blue blowfly).

Bukaryota Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
Calliphoridae; Calliphora.
PROSITE; PS00173; XYLOSE ISOMERASE 2; PARTIAL.
Isomerase; Pentose shunt; Xylose metabolism; Metal-binding; Magnesium.
NON TER 9 9
SEQÜENCE 9 AA; 983 MW; F64BAIEDC5B87DDI CRC64:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20564325; PubMed=10988292; Balaji R.A., Ohtake A., Sato K., Gopalakrishnakone P., Kini R.M., Seow K.T., Bay B.-H., i was been family of conotoxins with unique disulfide pattern and protein folding. Isolation and characterization from the
                                                                                                                                                                    Gaps
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Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 22.2%; Score 16; DB 1; Length 11; Best Local Similarity 42.9%; Pred. No. 5.7e+03; Matches 3; Conservative 0; Mismatches 4; Indels
                                                                                                                    22.2%; Score 16; DB 1; Length 9; 60.0%; Pred. No. 1.4e+05; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P58809;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
18-FEB-2003 (Rel. 41, Last annotation update)
Lambda-conotoxin CMrX.
                                                                                                                                                                                                                                                                                                                                                                                                             01-NoV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Callitachykinin II.
                                                                                                                                                                                                                                                                                                                                                                        11 AA.
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                                                                                                                      Query Match
Best Local Similarity 60.0
Matches 3; Conservative
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5 SAHTF 9
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P41518;
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CXL3_CONMR
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TKC2_CALVO
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Sakagami Y., Yoshida M., Isogai A., Suzuki A.;
Sakagami Y., Yoshida M., Isogai A., Suzuki A.;
Peptide sex hormones inducing conjugation tube formation in
compatible mating-type cells of Tremella mesenterica.";
Science 212:1525-1527(1981)
-! FWATION: Tremerogen A-10 is produced by the a mating-type cells
and induces formation of conjugation tubes in a mating-type cells.
PIR; A01642; JTUG0.
DIR; A01642; JTUG0.
S-12-hydroxyfarnesyl cysteine.
METHYLATION.
MDD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Fungi, Basidiomycota, Hymenomycetes, Heterobasidiomycetes,
Tremellomycetidae, Tremellales, Tremellaceae, Tremella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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venom of Conus marmoreus.";

J. Biol. Chem. 275:39516-39522 (2000).

-!- FUNCTION: Inhibits the neuronal noradrenaline transporter.
-!- SUBCELIULAR LOCATION: Secreted.
-!- TISSUB SPECIFICITY: Expressed by the venom duct.
-!- MASS SPECTROMETRY: MW=1262.77; MW ERR=0.07; METHOD=Electrospray.
-!- SMILLARITY: Belongs to the chi/lambda-conotoxin family.

Neurotoxin; Toxin; Hydroxylation.
DISULFID 4 9
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01-DEC-1992 (Rel. 24, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Alpha-conotoxin SIA (SIA).
Conus striatus (Striated cone).
Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
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Pred. No. 6.2e+03;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                              Score 16; DB 1; Length 12;
Pred. No. 6.2e+03;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                      HYDROXYLATION.
277AAE2422D5A2C8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12 AA.
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50.0%;
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12 AA; 1251 MW;
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Best Local Similarity 66.7%;
Matches 2; Conservative
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Best Local Similarity 50.v...
Best a 2; Conservative
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MEDLINE=91369955; PubMed=1892838;

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                              "Alpha-conotoxins, small peptide probes of nicotinic acetylcholine
                                                                                         -!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUB SPECIFICITY: Expressed by the venom duct.
-!- SIMILARITY: Belongs to the conotoxin A-superfamily. Alpha-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Purification and characterization of bioactive peptides from skin
                                                                                                                                                                                                                                                                                                                                                                                             Rana esculenta (Edible frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea, Ranidae, Rana.
                                                                                                                                                                                                                                              0
                                                            -!- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, bind to the nicotinic acetylcholine receptors (nAChR) and inhibit them.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Skin secretion,
MEDLINE=90198965, PubMed=2317508;
Simmaco M., de Biase D., Severini C., Aita M., Erspamer G.F.,
Barra D., Bossa F.;
         Myers R.A., Zafarella G.C., Gray W.R., Abbot J., Cruz L.J.,
                                                                                                                                                                                                                    22.2%; Score 16; DB 1; Length 13; 37.5%; Pred. No. 6.7e+03; 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 16; DB 1; Length 13;
Pred. No. 6.7e+03;
0; Mismatches 2; Indels
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DEF1931982457EBD CRC64;
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Amphibian defense peptide; Amidation; Hemolysis.
                                                                                                                                                                                                                                                                                                                                                     01-0CT-1993 (Rel. 27, Created)
01-0CT-1993 (Rel. 27, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Hemolytic protein B9 (Fragment).
                                                                                                                                PIR; A40312; NTKNAS.
Postsynaptic neurotoxin; Neurotoxin; Toxin;
Acetylcholine receptor inhibitor; Amidation.
                                                                                                                                                                                                                                                                                                                                      13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            extracts of Rana esculenta.";
Biochim. Biophys. Acta 1033:318-323(1990).
-!- FUNCTION: Shows hemolytic activity.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Skin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AMIDATION.
                                                   Biochemistry 30:9370-9377(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22.2%;
66.7%;
                                                                                                                                                                                                13 AA; 1461 MW;
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Best Local Similarity 37.50,
Tonservative
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                     ivera B.M.;
                                                                                                                                                                                                                                                                                                                                    RANES
                                                                                                                           family
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HPB9_RANES
ID HPB9_RANI
AC P32416;
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SPECIES=C.maenas, TISSUE=Pericardial organs, Stangler J., Hilbich C., Beyreuther K., Keller R., William Cardioactive peptide (CCAP) from pericardial organs of the shore crab Carcinus maenas.", Proc. Natl. Acad. Sci. U.S.A. 84:575-579(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=93050243; PubMed=1426284;
Cheung C.C., Loi P.K., Sylwester A.W., Lee T.D., Tublitz N.J.;
"Primary structure of a cardioactive neuropeptide from the tobacco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
0
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Eumalacostraca; Eucarida; Decapoda; Pleccyemata; Brachyura;
Eubrachyura; Portunoidas; Portunidae; Carcinus.
NCBL_TaxID=6759, 7130, 7067, 37547;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPECIES=T.molitor, and S.eridania; TISSUE=Head;
MEDILINE=94176032; PubMed=8129851;
Furnya K., Liao S., Reynolds S.E., Ota R.B., Hackett M.,
Schooley D.A.
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                                                                                                    Carcinus maenas (Common shore crab) (Green crab),
Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm),
Tenebrio molitor (Yellow mealworm), and
Spodoptera eridania (Southern armyworm).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 9 AA; 959 MW; C5A861A9CDD44EB9 CRC64;
01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Cardioactive peptide (CCAP).
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100.0%; Prev
0; N
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FEBS Lett. 313:165-168(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR, A26363; A26363.
PIR, S27233; S27233.
Neuropeptide; Amidation.
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nes 2; Conservative
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PRT;

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RESULT 15 CCAP CARMA ID CCAP CARMA AC P38556;

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September 5, 2004, 10:22:06; Search time 57 Seconds (without alignments) 71.960 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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sp_virus:*
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sp_unclassified:*
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1: sp_archea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Score 27; DB 13; Length 13; Pred. No. 3.6e+02; 0; Mismatches 2; Indels

Query Match
Best Local Similarity 75.0%;
Matches 6; Conservative

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Q37925 bacteriopha Q9ps71 agkistrodon Q7y846 ovis aries Q7y849 ribes divar Q9udc6 homo sapien P82881 rana clamit Q9uc13 secherichia Q9hc13 homo sapien Q8t0y6 apis mellif Q9bfr4 myrmecophag Q7ykc9 ribes speci Q13377 homo sapien Q35758 rattus norv Q7x139 staphylococ Q30790 erwinia amy Q1599 homo sapien Q88612 middelburg Q8ney9 homo sapien Q9ruf drosophila Q6424 rattus sp. Q9me9 homo sapien Q9666 homo sapien Q9666 homo sapien Q9666 homo sapien Q9666 homo sapien	PRT; 13 AA. reated) ast sequence update) ast sequence update) ast annotation update) cotein (Fragment). rrish) (Takitugu rubripes). craniata; Vertebrata; Euteleostomi; Teleostei; Bueleostei; Neoteleostei; i) Percomorpha; Tetraodontiformes; ii) Percomorpha; Tetraodontiformes; ii) Percomorpha; Tetraodontiformes; ii) Percomorpha; Tetraodontiformes; iii) iii) in the Japanese puffer fish pact vertebrate genome."; seducer activity; IEA. seducer activity; IEA. coupled receptor protein signalin; IEA.
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Q918T4;

RESULT 2

Q918T4

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MEDLINE=92031443; PubMed=1931944; Garabalant R.G.; Medine R.G.; Yount R.G.; Tount R.G.; Solitant R.G.; Solitant
                                                        Gallus gallus (Chicken).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=83017877; PubMed=7123853;
MEDLINE=83017877; PubMed=7123853;
Maillard R.K., Li J.K., Keene J.D., Joklik W.K.;
Gaillard R.K., Li J.K., Keene J.D., Joklik W.K.;
sequences at the termini of four genes of the three reovirus serotypes.";
Virology 121:320-326(1982).
EMBL; J02323; AAA47259.1; -.
NON TER 12
SEQÜENCE 12 AA, 1275 MW; 4B292B17FCB9C873 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=83017876; PubMed=6927854;
Antczak J.B., Chmelo R., Pickup D.J., Joklik W.K.;
"Sequences at both termini of the 10 genes of recovirus serotype
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 23, DB 13, Length 12;
Pred. No. 1.9e+03;
1; Mismatches 3; Indels
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Last annotation update)
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Reovirus serotype 3 M3 (Fragment).
Reovirus (type 3 / strain Dearing).
Viruses; dsRNA viruses; Reoviridae; Orthoreovirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31.9%;
Local Similarity 55.6%;
Les 5; Conservative
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Virology 121:307-319(1982).
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Matches 6; Conservative
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                                                                                                                                                                                                                 NCBI_TaxID=9031;
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Q9GJU2;
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STEALUR—HPU16E2CC6;
Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
"Sequence variation and physical state of human Papillomavirus type 16
"Sequence variation and physical state of human Papillomavirus type 16
"Sequence variation and physical state of human Papillomavirus
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Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
"Sequence variation and physical state of human Papillomavirus type 16
cervical cancer isolates from Australia and New Caledonia.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF407220; AAL01406.1; -.
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Pred. No. 5.6e+02;
2; Mismatches 1; Indels
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
                                                                                                                                                                                                                                                                                                                                                                           Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
NCBI_TaxID=10581;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
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llarity 54.5%; Pred. No. 5.6e+02;
Conservative 2; Mismatches 1;
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Similarity 54.5%;
6; Conservative 2
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les 6; Conserv
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SEQUENCE
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RESULT 4 Q9PS67

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GORAYA J., Knoop F.C., Conlon J.M., "Ranatuerins: antimicrobial peptides isolated from the skin of the American bullfrog, Rana catesbelana.";
Blochem. Blochem. Blochem. Bsophys. Res. Commun. 256:589-522(1998).
                                                                                                                                                                                              Score 21; DB 13; Length 13;
Pred. No. 5e+03;
0; Mismatches 1; Indels
                                                                                                                                                                      C85480B95DF885BD CRC64;
                                                                                                                                           GO; GO:0006805; P:xenobiotic metabolism; IEA. Antibiotic.
                                                                                                                               -!- SUBCELLULAR LOCATION: SECRETED
                                              MEDLINE=98422096; PubMed=9751476;
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(TrEMBLrel, 13, I
(TrEMBLrel, 19, I
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NON TER 1
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Best Local Similarity 83.3
Matches 5, Conservative
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Best Local Similarity
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                                   TISSUE=SKIN;
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01-DEC-2001
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0
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                                                                                SEQUENCE FROM N.A.

Nonneman D., Geesink G.H., Koohmaraie M.;

"Differential splicing and protein isoforms of ovine calpastatin.";

Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF192536; AAG31688.1;

EMBL; AF192535; AAG31687.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                    Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Calpastatin (Fragment).
Ovis aries (Sheep).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea, Ranidae, Rana.
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Skarzycia, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
NCBI_TaxID=8400;
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Pred. No. 5e+03;
0; Mismatches 1; Indels
                                                                                                                                                                                                Score 21; DB 6; Length 13; Pred. No. 5e+03;
                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                      13 AA; 1335 MW; 47E9542C696BADD3 CRC64;
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Last annotation update)
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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GO; GO:0006805; P:xenobiotic metabolism; IEA.
Antibiotic.
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80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                     Rana catesbeiana (Bull frog)
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                                                                                                                                                                               Query Match
Best Local Similarity 80.00,
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                                                 Bovidae; Caprinae; Ovis.
NCBL_TaxID=9940;
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                                                                                                                                                                                                                                                                  GKSTS 13
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RANATUERIN 7.
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SEQUENCE
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P82821
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Cryptococcus neoformans var. neoformans.
Bukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
NCBL_TaxID=40410;
                                                                                                                                                        Eukaryota; Viridiplantae: STreptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Brassica.
NCBI_TaxID=3712;
                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-99264316; PubMed=10330480;
Cabrillac D., Delorme V., Garin J., Ruffio-Chable V., Giranton J.L.,
Dumas C., Gaude T., Cock J.M.;
The S15 self-incompatibility haplotype in Brassica includes three S
gene family members which are expressed in stigmas.";
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Pred, No. 6.5e+03;
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                             01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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Last annotation update)
  11 AA
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PRT;
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                                                                                                                                      Brassica oleracea (Cauliflower).
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Query Match
Best Local Similarity
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SEQUENCE
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                        STRAIN=CBS884, BAL 3, and CBS6989;
MEDLINE=99380307; PubMed=10449476;
Halliday C.L., Bui T., Krockenberger M., Malik R., Ellis D.H.,
Carter D.A.;
"Presence of alpha and a mating types in environmental and clinical
collections of Cryptococcus neoformans var. gattii strains from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=98422096; PubMed=9751476; Gordon J.M.; Gordon J.M.; Knoop F.C., Conlon J.M.; Gordon J.M.; Manatuerins: antimicrobial peptides isolated from the skin of the American bullfrog, Rana catesbeiana."; Biochem. Biophys. Res. Commun. 250:889-592(1998).
- I. SUBCELLULAR LOCATION: SECRETED. SEQUENCE 12 AA; 1335 MW; C853ID12A92735BD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rana catesbeiana (Bull frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea, Ranidae; Rana.
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                                                                                                                                                                                                                                                                                                 12 AA; 1307 MW; 5AF9B485D5A735B7 CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
GTP-binding protein Golf alpha subunit (Fragment).
G<ALPHA>OLF
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
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                                                                                                                                                      Australia.";
J. Clin. Microbiol. 37:2920-2926 (1999).
BMBL; AR155349; AAF20374.1; -.
BMBL; AR155347; AAF20372.1; -.
BMBL; AR155348; AAF20373.1; -.
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SEQUENCE FROM N.A.
MEDLINE=96115117; PubMed=7494450;
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Matches 5; Conserv
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"Ranatuerins: antimicrobial peptides isolated from the skin of the American bullfrog, Rana catesbelana.";
Biochem. Biophys. Res. Commun. 250:589-592(1998).
-i. FUNCTION: ANTIBACTERIAL PEPTIDE AGAINST GRAM-NEGATIVE BACTERIUM S. AUREUS.
Herve D., Rogard M., Levi-Strauss M.; "Molecular analysis of the multiple Golf alpha subunit mRNAs in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NJV-1996 (TrEMBLrel. 01, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
N-acetylglucosamine (Betal-4) galactosyl transferase (EC 2.4.1.90)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rana catesbeiana (Bull frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
NCBI_TaxID=8400;
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                                                                                                                                                                                 Score 20; DB 11; Length 13; Pred. No. 7.7e+03;
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                                                                                                                                      0B6E3319671CA5B4 CRC64;
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Last annotation update)
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57.1%;
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EMBL; D00315; BAA00217.1; -.
GO; GO:0003945; F:N-acetyllactosamine synthase activity; IEA.
GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.
Glycosyltransferase; Transferase.
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SEQUENCE 12 AA; 1283 MW; 304EA40668387728 CRC64;
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Prolactin (Fragment).
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Musinae
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SEQUENCE FROM N.A.
Harigaya T., Imai H.;
Harigaya T., Imai H.;
Fartial nucleotide sequence of mouse prolactin gene, intron2.";
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AB011669; BAA25091.1;
NON TER
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SEQUENCE 13 AA; 1441 MW; 0B043BS0DD1545B4 CRC64;
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26.4%; Score 19; DB 11; Length 13;
Best Local Similarity 50.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 1; Mismatches 2; Indels
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004s:*

SUMMARIES

	Description	Annotation Apply Apply VEG has	VECT	VEGE	VEGF	VEGE	Felin			HLA CL		TmmT	_	Aab10896 Human 907					Abi04570 Bone marx				Hilman	DPT tr		Aali/6477 Denreggio
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ADA23476	AAB26567	AAU16900	ABJ00485	ABJ04090	ABJ04092	ABJ04093	AAU08458	AAW83264	AAW67159	AAW97980	AAY76718	ABP74688	ADC09547	AAG84316	AAG96997	AAG96549	ABP47552	ABP74689	ADC09548	
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12	13	13	13	13	13	13	80	σ	σ	6	60	σ	σ	10	10	10	10	10	10	
37.5	37.5		37.5		37.5	37.5	36.1	36.1	36.1	36.1	36.1	36.1	36.1	36.1	36.1	36.1	36.1	36.1	36.1	
27	27	27		27		27		26	56	26	56			56	56		56	26	26	
26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

Æ. VEGF based monocyclic peptide 1. AAU04524 standard; peptide; 13 (first entry) 26-SEP-2001 AAU04524; RESULT 1

Human; VEGF; vascular endothelial growth factor; angiogenesis; neovascularisation; lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic. Location/Qualifiers Synthetic Кеу

/note= "This bond cyclises the peptide" Disulfide-bond WO200152875-A1

26-JUL-2001

18-JAN-2000; 2000US-0176293P. 16-MAY-2000; 2000US-0204590P.

18-JAN-2001; 2001WO-US001533

(LUDW-) LUDWIG INST CANCER RES

Cendron A; Stacker S, Achen MG, Hughes RA,

WPI; 2001-442248/47

Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine residues

Claim 49; Page 32; 102pp; English.

The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human VEGPD (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring betabeta carbon separation distances on opposite antiparallel strands of a

CASELGKSTNTFC 13 US-09-761-636A-5 score: Sequence:

³⁸³⁹⁰⁴ Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 13 Minimum DB Maximum DB

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cyclising the peptide by oxidising the cysteine residues. The monocyclic cyclising the peptides (comprising 2 linked monocyclic peptides) dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with angiogenesis, concaveration or lymphangiogenesis in a mammal with a condition characterised by angiogenesis, neovascularisation or lymphangiogenesis. The condition is diabetic retinopathy, psoriasis, arthropathy, cerebrovascular accident, post-angioplasty restenosis, head, heat or cold tramma, substance-induced neovascularisation of the liver, excessive cramma, substance-induced neovascular sequelae, hypertension induced neovascular sequelae, or chronic liver sequelae, hypertension induced neovascular sequelae, or chronic liver care sequelae, hypertension induced neovascular sequelae, or chronic liver care infection. The peptides are also used to modulate vascular permeability or brain. The peptides are used to inage blood vessels and lymphatic or brain. The peptides are used to inage blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are used to interfere with at least one biological activity induced by VEGF, VEGF-C or D and care also used in combination with an anti-inflammatory agent, to treat a continuous control archivity induced by VEGF, VEGF-C or D and care also used in combination with an anti-inflammatory agent, to treat a chronic inflammation, when an anti-inflammatory agent, to treat and care also used in combination with an anti-inflammatory agent, to treat a chronic inflammation with an anti-inflammatory agent, to treat and also used in combination with an anti-inflammatory agent, to treat and also used in combination with an anti-inflammatory agent, to treat and also used in combination with an anti-inflammatory agent, to treat and also used in combination with an anti-inflammatory agent, to treat and also used in combination with an anti-inflammatory agent, to trea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human, VEGF; vascular endothelial growth factor; angiogenesis; neovascularisation; lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 72; DB 4; Length 13: 100.0%; Pred. No. 2.1e-05; Udels
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/note= "This bond cyclises the peptide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU04534 standard; peptide; 13 AA
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16-MAY-2000; 2000US-0204590P.
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nes 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diabetic retinopathy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200152875-A1
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Matches
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The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human whose 3-dimensional structure is modelled on the expose loop of human USGPD (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring beta-cc peptide loop fragment from an exposed loop of a growth factor protein and cyclis peptides by oxidising the peptide by oxidising the peptide of comprising 2 linked monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior corpitation are used to interfere with angiogenesis.

CC cyclisation are used to interfere with angiogenesis.

CC croyalisation are used to interfere with angiogenesis.

CC croyalisation is diabetic retinopathy, peoriasis, arthropathy, cerebrovascular accident, post-angioplasty restenosis, head, heat or cold trauma, substance-induced neovascularisation or lymphangiogenesis.

CC frauma, substance-induced neovascular sequelae, nypertension induced neovascular sequelae, hypertension induced neovascular sequelae, nypertension induced neovascular sequelae, hypertension induced neovascular sequelae, nypertension induced neovascular sequelae, nypertension induced neovascular sequelae, or chronic liver infection. The peptides are also used to modulate vascular permeability in a communation in peripheral limbs or in lungs, peritone and lymphatic corputation in peripheral limbs or in lungs, peritone and lymphatic corputation with an anti-inflammatory agent, to treat a chronic inflammation with an anti-inflammatory agent, to treat a chronic inflammation with an anti-inflammatory agent, to treat a chronic inflammation with an anti-inflammatory agent, to treat a chronic inflammation with an anti-inflammatory agent, to treat a corput corputation in peripheral activity induced by VEGF.
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Pred. No. 6.8e-05;
1; Mismatches 0; Indels

    13
/note= "This bond cyclises the peptide"

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                                       Example 25; Page 47; 102pp; English.
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16-MAY-2000; 2000US-0204590P.
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Query Match

Best Local Similarity

""a 12; Conservative
""ar 13
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Gaps ö

Length 13;

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Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine
                                                                    Example 25; Page 47; 102pp; English.
(LUDW-) LUDWIG INST CANCER RES.
                         WPI; 2001-442248/47
             Achen MG,
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The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human control of vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring beta-beta carbon separation distances on opposite antiparallel strands of a beta carbon separation distances on opposite antiparallel strands of a cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides and a cyclic peptide with at least one amino acid deleted prior cyclisation are used to interfere with angiogenesis, covascularisation or lymphangiogenesis and mammal with a condition cyclisation or lymphangiogenesis, arthropathy, nemangioma, vascularised malignant or benign tumour, post-recovery carbovascular acident, post-angioplasty restenosis, head, heat or cold trauma, substance-induced neovascularisation of the liver, excessive conference in difference induced neovascular sequelae, hypertension induced neovascular sequelae, or chronic liver in fertion. The peptides are also used to modulate vascular permeability accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, or bright at least one biological activity induced by VEGF-C or -D and chronic inflammation, especially rheumatoid arthritis, psociasis and chronic retinonathy Gaps .; 0 Score 65; DB 4; Length 13; Pred. No. 0.00033; 2; Mismatches 0; Indels 90.3%; 11; Conservative diabetic retinopathy Local Similarity Sequence 13 AA; Query Match Matches

1 CASELGKSTNTFC 13 1 CASELGKTSNTFC 13 ð

.; 0

AAU04537 standard; peptide; 13

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26-SEP-2001 (first entry)

Human; VEGF; vascular endothelial growth factor; angiogenesis; neovascularisation; lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic. VEGF based monocyclic peptide 15.

Synthetic

/note= "This bond cyclises the peptide" Location/Qualifiers Disulfide-bond

WO200152875-A1

26-JUL-2001

Cendron A;

Stacker S,

Hughes RA,

18-JAN-2001; 2001WO-US001533.

18-JAN-2000; 2000US-0176293P.

16-MAY-2000; 2000US-0204590P.

(LUDW-) LUDWIG INST CANCER RES

Cendron A; Stacker S, Hughes RA, Achen MG,

WPI; 2001-442248/47.

Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine residues.

Example 25; Page 47; 102pp; English.

The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human vector (wascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring betact carbon separation distances on opposite antiparallel strands of a peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with angiogenesis, neovascularisation or lymphangiogenesis in a mammal with a condition characterised by angiogenesis, neovascularisation or lymphangiogenesis.

The condition is diabetic retinopathy, psoriasis, arthropathy, corphyronaccial and account of the condition of the co Cerebrovascular accident, mailigiant to relight the condition of the liver, become trauma, substance-induced neovascularisation of the liver, excessive hormone-related angiogenic dysfunction, diabetes induced neovascular sequelae, hypertension induced neovascular sequelae, hypertension induced neovascular sequelae, or chronic liver infection. The peptides are also used to modulate vascular permeability an amammal has a condition characterised by fluid or brain. The peptides are used to image blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are used to interfere with at least one biological activity induced by VEGF, VEGF-C or -D and are also used in combination with an anti-inflammatory agent, to treat abronic inflammation, especially rheumatoid arthritis, psoriasis and diabetic retinopathy

Sequence 13 AA;

. 90.3%; Score 65; DB 4; Length 13; 84.6%; Pred. No. 0.00033; ive 2; Mismatches 0; Indels Conservative Local Similarity les 11; Conserv Query Match Matches

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Gaps

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AAU04536 standard; peptide; 13 AA. AAU04536; RESULT 5 AAU04536 MAXEX BX AX AX

(first entry) 26-SEP-2001

VEGF based monocyclic peptide 14.

Human; VEGF; vascular endothelial growth factor; angiogenesis; neovascularisation; lymphangiogenesis; psoriasis; tumour;

Feline immunodeficiency virus; FIV; infection; diagnosis; gpl30; p55; immunogenic fragment; antibody; env precursor; gag precursor; cat; antibody binding composition.

Feline immunodeficiency virus

EP962774-A1 08-DEC-1999 99EP-00303760. 98US-0085615P

14-MAY-1999; 15-MAY-1998; 03-JUN-1998;

Feline immunodeficiency virus env precursor peptide #2.

(first entry)

21-FEB-2000

AAY57039

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Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine
diabetes induced neovascular sequelae, rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic.

    13 /note= "This bond cyclises the peptide"

                                                                                                                                                                                                                                                       Example 25; Page 47; 102pp; English.
                                          Location/Qualifiers
                                                                                                                                                                           Stacker S,
                                                                                                                                                           (LUDW-) LUDWIG INST CANCER RES
                                                                                                                18-JAN-2001; 2001WO-US001533.
                                                                                                                                 18-JAN-2000; 2000US-0176293P
                                                                                                                                        16-MAY-2000; 2000US-0204590P.
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ses 10; Conservative
                                                                                                                                                                           Hughes RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diabetic retinopathy
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                                                    Disulfide-bond
                                                                              WO200152875-A1
                                                                                               26-JUL-2001
                            Synthetic
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Diagnosing Feline Immunodeficiency Virus infection

Claim 6; Page 9; 15pp; English.

O'connor

Mermer B,

Groat RG,

WPI; 2000-025671/03

(IDEX-) IDEXX LAB INC.

Cendron A;

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44.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human whose 3-dimensional structure is modelled on the expose loop of human (WGSPD (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring beta-comparing the comparing the peptide by oxidising the peptide by oxidising the peptide by oxidising the proposite autiparallel strands of a peptide loop fragment from an exposed loop of a growth factor protein and comparing the comparising 2 linked monocyclic peptides, and a cyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior comparation are used to interfere with angiogenesis.

CC cyclisation are used to interfere with angiogenesis.

CC covascularisation or lymphangiogenesis in a mammal with a condition characterised by angiogenesis, neovascularisation or lymphangiogenesis.

CC fracebrowascular accident, post-angioplasty restenosis, head, heat or cold crecebrowascular accident, post-angioplasty restenosis, head, heat or cold crecebrowascular accident, post-angioplasty restenosis, head, heat or cold crecebrowascular accident daysfunction, diabetes induced neovascular sequelae, hypertension induced neovascular sequelae, or dirronic liver infection. The peptides are also used to modulate vascular permeability cor brain. The peptides are used to image blood vessels and lymphatic cor brain. The peptides are used to image blood vessels and lymphatic corputation in peripheral limbs or in lungs, peritoneal cavity, pleura, accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, caccumulation in peripheral limbs or in lungs peripheral activity induced by VEGF Cor D and are also used in combination with an anti-inflammatory agent, to treat a corputation inflammation, especially rheumatoid arthritis, psoriasis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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Pred. No. 0.0016;
3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84.7%;
76.9%;
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AAY57039 standard; peptide; 12 AA.

AAYS7039 ID AAYS RESULT 6

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This sequence is a fragment of feline immunodeficiency virus (FIV) glycoprotein 130. Peptides AAY57038-Y57039 are used in the invention as capture polypeptides when diagnosing FIV infection. The invention relates to an antibody binding composition which consists of an enhanced capture polypeptide, which contains an immunogenic fragment of FIV gag precursor p55, and a second fragment which is part of the env precursor gp130, and an antibody-binding detection composition. The invention also includes a device for performing an assay which determines whether a feline is infected with FIV. The novel method is used for the diagnosis of Feline Immunodeficiency Virus infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Immunoglobulin binding peptide; autoimmune disease; rheumatoid arthritis; multiple sclerosis; myasthenia gravis; immunosuppressive; antirheumatic;
                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                           .;
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                                                                                                                                                                                                                                                                                                                                    Score 32; DB 3; Length 12;
Pred. No. 1.3e+02;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunoglobulin binding peptide #14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABJ04094 standard; peptide; 13 AA
                                                                                                                                                                                                                                                                                                                                                                                           1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200238592-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
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antigen receptor V-beta chain CDR3 region sequences accumulated in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to peptide sequences present in the synovial fluid and membranes of rheumatoid arthritis patients, arising from the CDR region of oligoclonal pathogenic T-cell antigen receptor Vbeta chains. Compositions which contain autoantigenic peptides binding specifically to
                                                                                                                                             New immunoglobulin-binding peptides, useful for removing autoantibodies from serum, e.g. for treating rheumatism, also related solid phases.
                                                                                                                                                                                                         The present invention relates to immunoglobulin binding peptides. These can be used to remove autoantibodies from solutions, particularly autoantibodies associated with autoimmune diseases such as rheumatism, multiple sclerosis and mysathenia gravis, from body fluids. The present sequence is a peptide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   atoid arthritis; arthrosis deformans; T-cell antigen receptor; chain; autoantigen; immunological tolerance.
                                                                                                                                                                                                                                                                                                                 Score 32; DB 5; Length 13;
Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          synovial membranes of rheumatoid arthritis patients.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T cell antigen receptor Vbeta 5 chain peptide.
                                                                                            Kunze R;
                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                          New immunoglobulin-binding peptides,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 3; Page 25; 136pp; Japanese.
                                                                                           Roenspeck W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY66781 standard; peptide; 13 AA.
                                                                (AFFI-) AFFINA IMMUNTECHNIK GMBH
                                                                                                                                                                                 Claim 3; Page 40; 54pp; German.
             08-NOV-2001; 2001WO-EP012933.
                                      08-NOV-2000; 2000EP-00124418
                                                                                                                                                                                                                                                                                                                 44.48;
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                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                        Egner R, Winkler D,
                                                                                                                  WPI; 2002-557447/59
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                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                    CASELGK
                                                                                                                                                                                                                                                                                                                                                                                             CASHLGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAZ96511
                                                                                                                                                                                                                                                                                         Sequence 13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TORI ) TORII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9963084-A1
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                                                                                                                                                                                                                                                                                                                                            . 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY66781;
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                  include antigen-specific immunological tolerance to rheumatoid arthritis can be used for the treatment and prevention of rheumatoid arthritis. The invention can be used for the diagnosis, treatment and prevention of rheumatoid arthritis. Sequences AAY66771-958 represent peptides from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Diagnosing a disorder characterized by expression of a human cancer associated antigen precursor, comprises detecting interaction of an agent with a nucleic acid molecule encoding the antigen precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       precursor (I) coded by a NA Group 1 nucleic acid molecule (NI) comprising contacting the biological sample with an agent (A) that specifically binds to MI, (I) or its fragment, complexed with an human leukocyte antigen (HLA) molecule and determining the interaction between the agent therapy and vaccine production activity and can be used in gene therapy and vaccine production. The method can be used for treating a subject with a condition characterised by expression of (I) in cells of a subject. AAB75607 and AAB75608 represent proteins from human cancer also associated antigen precursors, and AAB75609 to AAB75802 represent HLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; cancer associated antigen precursor; cancer associated antigen; seminoma; HLA; human leukocyte antigen; cytostatic; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Characterised by expression of a human cancer associated antigen (CAA) precursor (I) coded by a NA Group 1 nucleic acid molecule (N1) compris
                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   class I binding motifs in human cancer associated antigen precursors given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes a method for diagnosing a disorder
                                                                                                                                                                                                      0
T-cells expressing receptors containing the peptide sequences,
                                                                                                                                                                  Length 13;
                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HLA class I binding motif in HOM-TES-84 SEQ ID NO:29.
                                                                                                                                              Score 30; DB 3; Len
Pred. No. 3 1e+02;
                                                                                         various Vbeta chains of T cell antigen receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 29; DB 4; I
Pred. No. 3.4e+02;
1; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfreundschuh M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 10; Page 62; 126pp; English
                                                                                                                                                                                                                                                                                                                                                              AAB75626 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-JUN-2000; 2000WO-US017207.
                                                                                                                                                               41.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                  5; Conservative
                                                                                                                                                                                                                                    1 CASELGKSTNTF 12
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Best Local Similarity 60.0
Matches 6; Conservative
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CASSIGTNNEQF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-112465/12.
                                                                                                                                                           Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vaccine; cancer.
                                                                                                                           Sequence 13 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                     10-APR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                 AAB75626;
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                                                                                                                                                                                                                                                                                                                          RESULT 9
AAB75626
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Gaps

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Gaps

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Immunoglobulin binding peptide; autoimmune disease; rheumatoid arthritis; multiple sclerosis; myasthenia gravis; immunosuppressive; antirheumatic; neuroprotective.
                                                                                                                                                                                                                                                                                                                                       The present invention relates to immunoglobulin binding peptides. These can be used to remove autoantibodies from solutions, particularly autoantibodies associated with autoimmune diseases such as rheumatism, multiple sclerosis and myasthenia gravis, from body fluids. The present sequence is a peptide of the invention
                                                                                                                                                                                                                                                                           New immunoglobulin-binding peptides, useful for removing autoantibodies from serum, e.g. for treating rheumatism, also related solid phases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homing peptide; organ; tissue; lung; pancreas; skin; retina; MDP; prostate; ovary; lymph node; adrenal gland; liver; gut; tumour; membrane dipeptidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                    40.3%; Score 29; DB 5; Length 13; 71.4%; Pred. No. 4.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                           Kunze
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                                                                                                                                                                                                                          Roenspeck W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY48678 standard; peptide; 9 AA.
                                                                                                                                                                                               (AFFI-) AFFINA IMMUNTECHNIK GMBH
                                                                                                                                                                                                                                                                                                                     Claim 3; Page 40; 54pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-00042107
99US-00258754
                                                                                                                                              08-NOV-2001; 2001WO-EP012933
                                                                                                                                                                      08-NOV-2000; 2000EP-00124418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 71.4
Matches 5, Conservative
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                                                                                                                                                                                                                          Egner R, Winkler D,
                                                                                                                                                                                                                                                      WPI; 2002-557447/59.
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                                                                                         WO200238592-A2
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26-FEB-1999;
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10-DEC-1999
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                                                                                                                  16-MAY-2002
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                                                                Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to peptide sequences present in the synovial fluid and membranes of rheumatoid arthritis patients, arising from the CDR region of oligoclonal pathogenic T-cell antigen receptor Vbeta chains. Compositions which contain autoantigenic peptides binding specifically to T-cells expressing receptors containing the peptide sequences, which include antigen-specific immunological tolerance to rheumatoid arthritis can be used for the treatment and prevention of rheumatoid arthritis. The invention can be used for the diagnosis, treatment and prevention of rheumatoid arthritis. Sequences ANY66771-958 represent peptides from the various Vbeta chains of T cell antigen receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T-cell antigen receptor V-beta chain CDR3 region sequences accumulated in synovial membranes of rheumatoid arthritis patients.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                              Rheumatoid arthritis; arthrosis deformans; T-cell antigen receptor; Vbeta chain; autoantigen; immunological tolerance.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 29; DB 3; Length 13;
Pred. No. 4.5e+02;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 13;
                                                                                                                                                                                       T cell antigen receptor Vbeta 10 chain peptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ¥
                                                                                                           AAY66787 standard; peptide; 13 AA
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Best Local Similarity 60...
6. Conservative
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N-PSDB; AAZ96517.
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                                                                                                                                                                                                                                                                                   WO9963084-A1
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                                                                                                                                                              11-APR-2000
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                                                                                                                                                                                                                                                                                                              09-DEC-1999
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                                                                                  RESULT 10
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WPI; 1999-571717/48.
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e.g. New peptides which selectively home to organs or tissues, used for, e.didentifying target ligands and for therapy of pathological conditions.

Example 6; Page 144; 193pp; English

The present invention describes peptides that selectively home to a tissue or organ. The peptides can be used for identifying an organ or tissue, for identifying a target molecule expressed by an organ or tissue or for treating an organ or tissue pathology, where the organ or tissue is selected from prostate, lung, skin, retina, pancreas, gut, ovary, adrenal gland, liver, and lymph node. The peptide bind to the membrane dipeptidase (MDP). AAV48018 to AAV49066 represent sequences which are used in the exemplification of the present invention. (Updated on 20-MAR-2003 to correct PR field.)

Sequence 9 AA;

ö 1; Indels Length 9; Score 28; DB 2; I Pred. No. 1.4e+06; 1; Mismatches 1; 38.9%; 71.4%; 5; Conservative Local Similarity Query Match Matches

7 KSTNTFC 13

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σ :|||| | 3 RSTNTGC

AAB10896 standard; protein; 9 AA.

AAB10896;

26-JAN-2001 (first entry)

Human 9D7 protein immunogenic fragment SEQ ID NO: 55.

Tumor-associated antigen; 9D7; human; cytostatic; immunogenic; immunotherapy; cancer; cellular anticancer vaccine; diagnostic; kidney; lung; colon; breast; carcinoma; Hodgkin's lymphoma.

Homo sapiens.

DE19909503-A1

07-SEP-2000

99DE-01009503, 04-MAR-1999;

99DE-01009503 04-MAR-1999; (BOEH) BOEHRINGER INGELHEIM INT GMBH.

Sommergruber W, Heider K; Klade C, Adolf G,

WPI; 2000-588357/56.

immunotherapy of cancer New tumor-associated antigen 9D7, useful e.g. for immur and for producing diagnostic or therapeutic antibodies.

Claim 6; Page 45; 50pp; German.

This invention describes a novel tumor-associated antigen, designated 9D7 which has cytostatic activity. The invention also describes a method for isolating (a) a polypeptide (I) that includes (SI) as part of its sequence; (b) an immunogenic protein fragment or peptide (II) derived from 9D7; (c) a pharmaceutical composition containing at least 1 of 9D7, I) or (II) as active ingredients; (d) an isolated DNA (III) encoding a protein (IV) with the immunogenic properties of 9D7 or its fragments; (e) a recombinant DNA (IIIa) that includes (III); and (f) antibodies (Ab) directed against 9D7, (I) or (II). 9D7, or its derived immunogenic

peptides, are used to induce a humoral and/or cellular response for use in in vivo or ex vivo immunotherapy of cancer. DNA (III) that encodes 9D7 can be used similarly and cells that express 9D7 are useful in cellular anticancer vaccines. Antibodies (Ab) specific for 9D7 are useful for imaging, diagnosing and monitoring cancers, also, when conjugated to cytotoxins or radiomuclide, as therapeutic agents. Peptides derived from 9D7 may also be used diagnostically to test for an immune response. 9D7-associated cancers are particularly kidney, lung, colon and breast carcinoma and Hodgkin's lymphoma. AAB10874 B10899 represent immunogenic fragments of the human tumor-associated antigen 9D7 which is described in the method of the invention 8X86888888888XX

Sequence 9 AA;

Gaps . Score 28; DB 3; Length 9; Pred. No. 1.4e+06; 0; Mismatches 2; Indels 38.9%; 5; Conservative Query Match Best Local Similarity Matches

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1 CASELGK 3 CGSRLGK ð

RESULT 14 AAE26783

0;

Gaps

AAE26783 standard; peptide; 9 AA.

AAE26783;

(first entry) 13-DEC-2002

Fibrin binding peptide #36

Fibrin binding peptide; thrombosis; pulmonary embolism; atherosclerosis; myocardial infarct; ischaemia; imaging; rheumatoid arthritis; vasotropic; anaemia; hypoxia; tumour; diabetic retinopathy; autoimmune disorder; inflammatory disorder; anglogenesis; stroke; cerebroprotective.

Unidentified

18-JUL-2002.

21-DEC-2001; 2001WO-US049534.

23-DEC-2000; 2000US-00747403

(DYAX-) DYAX CORP.

Beltzer JP, Wescott CR,

WPI; 2002-666875/71.

Novel synthetic fibrin-binding moiety, useful for detecting, imaging or localizing fibrin-containing clots by magnetic resonance imaging, radioimaging and for treating diseases involving thrombus formation e.g.

Claim 4; Page 55; 89pp; English.

The invention relates to a synthetic fibrin binding group having affinity for fibrin. The invention is useful for detecting fibrin in a mammalian subject which involves (a) detectably labelling the binding group; (b) administering to the subject the labelled polypeptide, and (c) detecting the labelled polypeptide in the subject. The invention is useful for treating a disease involving thrombus formation eg. deep-vein thrombosis, pulmonary embolism, cardiogenic thrombosis, atherosclerosis, myocardial infarct, reperfusion ischaemia or stroke. The binding moieties are useful for detection, imaging and localisation of fibrin-containing clots by magnetic resonance imaging, radioimaging and other imaging methods and are also useful in the diagnosis and treatment of coronary conditions where fibrin plays a role. The fibrin binding moieties are useful for

peptides, are used to induce a humoral and/or cellular response for use

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binding peptide
$$$$$$$$$$$$$$$$$$$$
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ucrecturing and ucaquious participates in which itemin prays a role eg. peritoneal adhesions which often occur after surgery or inflammatory and neoplastic processes and are comprised of a fibrin network, fibroblasts, macrophages and new blood vessels, theumatoid carthritis, lupus or septic arthritis which often have bits of fibrin containing tissues called rice bodies in the synovial fluid of their joints; thrombocytopenic purpura, a type of anaemia in which deposits in arterioles causes turbulent blood flow resulting in stress and destruction of red blood cells. The fibrin specific agents can also be used to detect hypoxia or ischaemia of heart, kidney, liver, lung, brain or or other organs, as well as the detection of tumours, diabetic retinopathy, early or high-risk atherosclerosis and other autoimmune and inflammatory disorders. Fibrin specific agents also could provide both direct or surrogate markers of disease models in which hypoxia and angiogenesis are expected to play a role. The invention is also useful for screening molecular libraries. The present sequence is a fibrin detecting and diagnosing numerous pathophysiologies in which fibrin plays

Sequence 9 AA;

ö ; 0 Score 28; DB 5; Length 9; Pred. No. 1.4e+06; Mismatches 2; Indel8 2; Mismatches 38.9%; 50.0%; Conservative Query Match Best Local Similarity Matches 4; Conserv Job time : 67 secs

6 GKSTNTFC 13 GOESRIFC 9

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RESULT 15

AAB10895 standard; protein; 10 AA. AAB10895;

26-JAN-2001 (first entry)

Human 9D7 protein immunogenic fragment SEQ ID NO: 54.

Tumor-associated antigen; 9D7; human; cytostatic; immunogenic; immunotherapy; cancer; cellular anticancer vaccine; diagnostic; kidney; lung; colon; breast; carcinoma; Hodgkin's lymphoma.

Homo sapiens.

DE19909503-A1

07-SEP-2000

99DE-01009503 04-MAR-1999; 99DE-01009503 04-MAR-1999; Sommergruber W, Heider K; Adolf G, Klade C,

(BOEH) BOEHRINGER INGELHEIM INT GMBH.

WPI; 2000-588357/56

New tumor-associated antigen 9D7, useful e.g. for immunotherapy of cancer and for producing diagnostic or therapeutic antibodies.

Claim 6; Page 45; 50pp; German.

This invention describes a novel tumor-associated antigen, designated 9D7 which has cytostatic activity. The invention also describes a method for isolating (a) a polypeptide (I) that includes (SI) as part of its sequence; (b) an immunogenic protein fragment or peptide (II) derived from 9D7; (c) a pharmaceutical composition containing at least 1 of 9D7, (I) or (II) as active ingredients; (d) an isolated DNA (III) encoding a protein (IV) with the immunogenic properties of 9D7 or its fragments; (e) a recombinant DNA (IIIa) that includes (III); and (f) antibodies (Ab) directed against 9D7, (I) or (II). 9D7, or its derived immunogenic

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    in in vivo or ex vivo immunocherapy of cancer. DNA [III] that encodes 907 can be used similarly and cells that express 907 are useful in cellular anticancer vaccines. Antibodies (Abb specific for 907 are useful for imaging, diagnosing and monitoring cancers, also, when conjugated to cytotoxins or radionuclide, as therapeutic agents. Peptides derived from 907 may also be used diagnostically to test for an immune response. 907-associated cancers are particularly kidney, lung, colon and breast carcinoma and Hodgkin's lymphoma. AAB10874-B10899 represent immunogenic fragments of the human tumor-associated antigen 907 which is described in
                                                                                                                                                                                                                                                                                                                                        ..
                                                                                                                                                                                                                                                                                           Score 28; DB 3; Length 10;
Pred. No. 5.1e+02;
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71.4%;
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Best Local Similarity
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September 5, 2004, 10:32:02; Search time 67 Seconds (without alignments) 61.132 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

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8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1298764 seqs, 315065143 residues
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72
1 CASELGKSTNTFC 13
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Perfect score:
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	Description	Momentum R Annual	Semience 3, Appil	Semience 15, Appl	Segment 19 Appl		Semience 17, Appl	, ,	* -	, i	Sequence 55, Appl	2	sednence II, Appl	Sequence 626. App	0	rddy 'or comonboa		sednence 262, App
SUMMARIES	B ID	9 US-09-761-636A-5	9 US-09-761-636A-15	9 US-09-761-636A-16	9 US-09-761-636A-18	9 US-09-761-636A-17	16 US-10-415-665-14	14 US-10-208-304-14	16 US-10-415-665-15	14 IIS-10-034-974-55	16 TIS=10-415-665-9			IO US-09-573-822C-626	14 US-10-271-343-19	10 US-09-791-393-262	10 TIS-09-791 01	797-696-161-60-03
	Query Match Length DB	100.0	5.8 13).3 13	0.3 13	84.7 13	44.4 13	41.7 10	40.3	38.9	9.9	38.9	, ,	. 01	7.5 10	7.5 12	7.5	
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US-09-142-613-22	US-10-014-340-84	62-527-2	-10-322-210-67	0-304-443-6	-10-415-665-	-10-415-66	US-10-415-665-13	US-09-795-006A-140	3-10-117-937-57	US-10-044-844-70	US-09-572-404B-2743	US-09-572-404B-3191	572-270A	-104-12	US-10-208-304-12	-304-1	-304 - 1	-10-208-304-1	-937-5	US-10-398-104-153	ď	US-10-415-665-82	à	US-10-415-665-66	US-10-415-665-74	-09-792-686A-	-217-1	-10-632-388-1	-10-651-723-17
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ALIGNMENTS

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Gaps
                                                                    APPLICANT: ACHEN, Marc
APPLICANT: ACHEN, Marc
APPLICANT: STACKER, Steven
APPLICANT: STACKER, Steven
APPLICANT: GENDRON, Angela
TITLE OF INVENTION: VECF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
FILE REFERENCE: 1064/48505 Achen et al
CURRENT APPLICATION NUMBER: US/09/761,636A
CURRENT APPLICATION NUMBER: US 60/176,293
PRIOR PILING DATE: 2000-101-18
PRIOR APPLICATION NUMBER: US 60/204,590
PRIOR PILING DATE: 2000-61-6
NUMBER OF SEO ID NOS: 34
SOUTHARD: Patentin version 3.0
SEQ ID NO 5
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100.0%; Pred. No. 6.6e-06;
iive 0; Mismatches 0;
                 ; Sequence 5, Application US/09761636A; Patent No. US20020065218A1; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
US-09-761-636A-5
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RESULT 2 US-09-761-636A-15

; Sequence 15, Application US/09761636A ; Patent No. US20020065218A1

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·: 0

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APPLICANT: Egner, Ralf
APPLICANT: Kunze, Rudolf
APPLICANT: Kunze, Rudolf
APPLICANT: Winkler, Dirk
APPLICANT: Wonspeck, Wolfgang
ITILE OF INVENTION: Peck ides, Preparation Thereof and Use Thereof for TITLE OF INVENTION: Bahding Immunoglobulins
FILE REFERENCE: P68842USO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INVOLVENTION:

APPLICANT: ACHEN, MARC
APPLICANT: STACKER, Steven
APPLICANT: STACKER, Steven
APPLICANT: CENDRON, Angela
APPLICANT: CENDRON, Angela
TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
FILE REFERENCE: 1064/48505 Achen et al
CURRENT APPLICATION NUMBER: US/09/761,636A
CURRENT FILING DATE: 2001-01-18
PRIOR APPLICATION NUMBER: US 60/176,293
PRIOR PLILING DATE: 2000-01-18
PRIOR FILING DATE: 2000-01-18
PRIOR FILING DATE: 2000-05-16
SPRIOR FILING DATE: 2000-05-16
SOFTWARE: PatentIn version 3.0
TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR FILE REFERENCE: 1064/48505 Achen et al CURRENT APPLICATION NUMBER: US/09/761,636A CURRENT PILING DATE: 2001-01-18 PRIOR APPLICATION NUMBER: US 60/176,293 PRIOR FILING DATE: 2000-01-18 PRIOR FILING DATE: 2000-06-16 NUMBER: OS SQ 1D NOS: 34 SOFTWARE: PATENTING DATE: 2000-06-16 NUMBER OF SEQ ID NOS: 34 SEQ ID NO 18 INDICATION OF SEQ ID NOS: 34 SEQ ID NO 18 INDICATION OF SEQ ID NOS: 34 SEQ ID NO 18 SEQ ID NO 1
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Pred. No. 0.00011;
2; Mismatches 0; Indels
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76.9%; Pred. No. 0.00059;
Live 3; Mismatches 0;
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CURRENT FILING DATE: 2003-10-16
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84.6%;
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; ORGANISM: synthetic construct
US-09-761-636A-17
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Matches 10; Conservative
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Best Local Similarity 84.6
Matches 11; Conservative
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Patent No. US20020065218A1

GENERAL INFORMATION

APPLICANT: ACHEN, Marc

APPLICANT: STACKER, Steven

APPLICANT: CENDRON, Angela

TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR

FILE REFERENCE: 1064/4865 Achen et al

CURRENT APPLICATION NUMBER: US 60/176,293

PRIOR APPLICATION NUMBER: US 60/176,293

PRIOR APPLICATION NUMBER: US 60/176,293

PRIOR APPLICATION NUMBER: US 60/204,590

PRIOR PILING DATE: 2000-01-18

PRIOR PLIING DATE: 2000-05-16

NUMBER OF SEQ ID NOS: 34

SOFTWARE: PATENTIN VUMBER: US 60/204,590

PRIOR FILING DATE: 2000-05-16

SOFTWARE: PATENTIN VUMBER: US 60/204,590

PRIOR DATE: 2000-05-16

SOFTWARE: PATENTIN VUMBER: US 60/204,590
                                                                     APPLICANT: ACHEN, MARC
APPLICANT: STACKER, Steven
APPLICANT: STACKER, Steven
APPLICANT: STACKER, Steven
APPLICANT: CENDRON, Angela
TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
FILE REFERENCE: 1064/48505 Achen et al
CURRENT FILING DATE: 2001-01-18
PRIOR APPLICATION NUMBER: US 60/176,293
PRIOR APPLICATION NUMBER: US 60/204,590
PRIOR FILING DATE: 2000-01-18
PRIOR PILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 15
LENGTH: 13
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Pred. No. 2.2e-05;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 95.8%;
Best Local Similarity 92.3%;
Matches 12; Conservative 1
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APPLICANT: STACKER, Steven
APPLICANT: HUGHES, Richard
APPLICANT: CENDRON, Angela
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US-09-761-636A-18
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Gaps

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TYPE: PRT

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CURRENT APPLICATION NUMBER: US/10/415,665
CURRENT FILING DATE: 2003-10-16
FRIOR APPLICATION NUMBER: PCT/FEP01/12933
FRIOR FILING DATE: 2001-11-08
FRIOR FILING DATE: 2000-11-08
NUMBER OF SEQ ID NOS: 88
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 15
LENGTH: 13
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Publication No. US20030143158A1
GENERAL INFORMATION:
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; Publication No. US20040087765A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 71.4%;
Matches 5; Conservative
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ORGANISM: Artificial Sequence
                      FILE REFERENCE: P68842US0
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2 CATHLGK 8
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Best Local Similarity
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Publication No. US20040087765A1
GENERAL INFORMATION:
APPLICANT: Egner, Ralf
APPLICANT: Kunze, Rudolf
APPLICANT: Kunze, Dirk
APPLICANT: Roenspeck, Wolfgang
TITLE OF INVENTION: Peptides, Preparation Thereof and Use Thereof for TITLE OF INVENTION: Binding Immunoglobulins
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i Sequence 14, Application US/10208304

i Sequence 14, Application US/10208304

i Publication No. US2030124571A1

i GENERAL INFORMATION:

APPLICANT: Larisch, Sarit

APPLICANT: Kim, Seonet J.

APPLICANT: Kim, Seonet J.

APPLICANT: Knoberts, Anita B.

APPLICANT: Y, Youngsuk

ITLE OF INVERTION: NOVEL HUMAN SEPTIN AND USES THEREFOR

ITLE OF INVERTION: NOVEL HUMAN SEPTIN AND USES THEREFOR

ITLE OF INVERTION: NOVEL HUMAN SEPTIN AND USES THEREFOR

ITLE OF INVERTION: NOVEL HUMAN SEPTIN AND USES THEREFOR

ITLE OF INVERTION NUMBER: US/10/208,304

CURRENT FILING DATE: 2002-07-29

PRIOR PILING DATE: 2000-01-29

PRIOR FILING DATE: 2000-01-29

PRIOR FILING DATE: 2000-01-29

PRIOR FILING DATE: 2000-12-29

NUMBER: OF SEQ ID NOS: 16

SOFTWARE: PATENTIN VERSION 3.1

SEQ ID NO 14

TUNDE: NUMBER: OF SEQ ID NOS: 16

SOFTWARE: PATENTIN VERSION 3.1

LENGITH: NO
                                                                                                                                                                                                                                                                                                                                                           44.4%; Score 32; DB 16; Length 13; 85.7%; Pred. No. 80; Live 0; Mismatches 1; Indels
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Pred. No. 1.4e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                           OTHER INFORMATION: Description of the artificial sequence:
OTHER INFORMATION: synthetic peptide having affinity for OTHER INFORMATION: immunoglobulins
US-10-415-665-14
PRIOR APPLICATION NUMBER: PCT/EP01/12933
PRIOR FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: EP00124418.5
PRIOR FILING DATE: 2000-11-08
NUMBER OF SEQ ID NOS: 88
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 14
LENGTH: 13
                                                                                                                                                                             TYPE: PRT ORGANISM: Artificial sequence
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87.58;
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Best Local Similarity 85.7:
...r.hes 6; Conservative
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Best Local Similarity 87.5
Matches 7; Conservative
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ORGANISM: Drosophila
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APPLICANT: Beltzer, James P.
APPLICANT: Beltzer, James P.
APPLICANT: Bescott, Charles R.
APPLICANT: Gato, Aaron K.
TITLE OF INVENTION: FIBRIN BINDING MOIETLES USEFUL AS IMAGING AGENTS
TITLE OF INVENTION: FIBRIN BINDING MOIETLES USEFUL AS IMAGING AGENTS
CURRENT APPLICATION NUMBER: US/10/034,974
CURRENT FILING DATE: 2000-12-23
FRIOR FILING DATE: 2000-12-23
NUMBER OF SEQ ID NOS: 56
SOFTWARE: Patentin version 3.1
SSQ ID NO 55
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APPLICANT: Winze, Rudolf
APPLICANT: Winzle, Dirk
APPLICANT: Winkler, Dirk
APPLICANT: Roenspeck, Wolfgang
IIILE OF INVENTION: Peptides, Preparation Thereof and Use Thereof for
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OTHER INFORMATION: Description of the artificial sequence: OTHER INFORMATION: synthetic peptide having affinity for OTHER INFORMATION: immunoglobulins
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| Sequence 11, Application US/10415665 | Publication No. US20040087765A1 |
| Sequence 11, Application US/10415665 | Publication No. US20040087765A1 |
| GENERAL INFORMATION: A PEPLICANT: Edner, Ralf |
| APPLICANT: Kunze, Rudoll |
| APPLICANT: Roenspeck, Wolfgang |
| TITLE OF INVENTION: Peptides, Preparation Thereof and Use Thereof for TITLE OF INVENTION: Peptides, Preparation Thereof and Use Thereof CURRENT APPLICATION NUMBER: US/10/415,665 |
| CURRENT APPLICATION NUMBER: US/10-16 |
| PRIOR FILING DATE: 2001-11-08 |
| PRIOR FILING DATE: 2001-11-08 |
| PRIOR FILING DATE: 2001-11-08 |
| NUMBER OF SEQ ID NOS: 88 |
| SOFTWARE: PatentIn Ver. 2.1
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OTHER INFORMATION: Description of the artificial sequence:
OTHER INFORMATION: synthetic peptide having affinity for
OTHER INFORMATION: immunoglobulins
                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Description of the artificial sequence: OTHER INFORMATION: synthetic peptide having affinity for OTHER INFORMATION: immunoglobulins
                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
      CURRENT APPLICATION NUMBER: US/10/415,665
CURRENT FILING DATE: 2003-10-16
PRIOR APPLICATION NUMBER: PCT/EP01/12933
PRIOR FILING DATE: 2001-11-08
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-08
NUMBER OF SEQ ID NOS: 88
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                 h 38.9%;
Similarity 71.4%;
5; Conservative (
                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Artificial sequence
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FILE REFERENCE: P68842US0
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Best Local Similarity
Matches 5; Conserv
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Best Local Similarity
Matches 5; Conserv
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US-09-573-822C-626
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LENGTH: 13
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TITLE OF INVENTION: Complementary peptide ligands generated from microbial genome seq
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US-09-573-822C-626
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; Sequence 19, Application US/10271343
; Publication No. US20030166003A1
; Publication No. US20030166003A1
; GENERAL INFORMATION: Andrea G.
; APPLICANT: Cochran, Andrea G.
; APPLICANT: Statovasnik, Melissa A.
; TITLE OF INVENTION: A STRUCTURED PEPTIDE SCAFFOLD FOR DISPLAYING TURN LIBRARIES
; TITLE OF INVENTION: ON PHAGE
; FILE REFERENCE: 11669-1164051
; CURRENT APPLICATION NUMBER: US/10/271,343
; CURRENT PILING DATE: 2002-10-15
; PRIOR PILING DATE: 1090-06-13
; PRIOR PILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 60
; SOFTWARR: PARENTIN VERSION 3.1
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                                                                                                                                                                                                                                                                                                                                                               Length 10;
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                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
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40.0%; Pred. No. 4.7e+02;
iive 5; Mismatches 1.
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                             FILE REFERENCE: Microbe patent
CURRENT APPLICATION NUMBER: US/09/573,822C
CURRENT FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 804
SOFTWARE: ProtPatent version 1.0
SEQ ID NO 626
LENGTH: 10
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COTHER INFORMATION: Xaa is D-pro
US-10-271-343-19
                                                                                                                                                                                                       TYPE: PRT
ORGANISM: mycoplasma genitalium
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Best Local Similarity 55.0
Langer 5, Conservative
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Matches 4; Conservative
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US-09-791-393-262
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US-10-271-343-19
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LENGIH: 10
                                                                                                                                                                                                                                                                                                                                                                      Query Match
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RESULT 15
US-09-791-389-262

i Sequence 262, Application US/09791389

i Publication No. US20030032773A1

i GENERAL INFORMATION:

APPLICANT: Herath, Herath Mudiyanselage Athula Chandrasiri

APPLICANT: Parekh, Rajesh Bhikhu

APPLICANT: Rohlff, Christian

APPLICANT: Ferrett, Jonathan Alexander

APPLICANT: Terrett, Jonathan Alexander

APPLICANT: Trerett, Jonathan Alexander

APPLICANT: Trerett, Jonathan Alexander

APPLICANT: Trerett, Jonathan Alexander

APPLICANT: Trerett, Jonathan Alexander

APPLICANT: Treson, Kerry Louise

ITILE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder

ITILE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder

ITILE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder

ITILE OF INVENTION: 2001-02-23

CURRENT APPLICATION NUMBER: US 0004412.3

PRIOR FILING DATE: 2000-02-24

PRIOR PILING DATE: 2000-12-08

SOFTWARE: FastSEQ for Windows Version 4.0

INWERN OF SEQ ID NOS: 308

SOFTWARE: FastSEQ for Windows Version 4.0
APPLICANT: Herath, Herath Mudiyanselage Athula Chandrasiri
APPLICANT: Parekh, Rajesh Bhikhu
APPLICANT: Parekh, Rajesh Bhikhu
APPLICANT: Parekh, Rajesh Bhikhu
APPLICANT: Robilff, Christian
TITLE OF INVENTION: Diagnosis and Their Use for
TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAD)
TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAD)
TITLE OF INVENTION: 2031-001 NUMBER: US/09/791,393
FILE REFERENCE: 253-1-001 NUMBER: US/09/791,393
CURRENT APPLICATION NUMBER: US/09/791,393
EARLIER APPLICATION NUMBER: GB 0030050.9
EARLIER PILING DATE: 2000-12-08
EARLIER PILING DATE: 2000-12-08
EARLIER FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 308
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 262
LENGTH: 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37.5%; Score 27; DB 10; Length 12; 57.1%; Pred. No. 5.7e+02; ative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 27; DB 10; Length 12;
Pred. No. 5.7e+02;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search completed: September 5, 2004, 10:37:18 Job time : 68 secs
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Best Local Similarity 57.1%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 37.5
Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
CORGANISM: homo sapien
US-09-791-393-262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: homo sapien
US-09-791-389-262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | :|||:
CTTELGR 12
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6 CTTELGR 12
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

September 5, 2004, 10:29:31; Search time 15 Seconds (without alignments) 44.743 Million cell updates/sec Run on:

72 1 CASELGKSTNTFC 13 Perfect score: Sequence:

Scoring table:

US-09-761-636A-5

Title:

389414 seqs, 51625971 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

127817 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 13

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

/cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:* Issued_Patents_AA:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Land & A apparent	6	93	N	'n	70	70,		219	219	170,	12. 7	m		2	116.	24.	183,	183,	11, 7	equence 183,	6. 4	è	,	. 65	-	151
SUMMARIES	ID	US-09-258-754-63	7	US-09-722-250D-63	US-07-732-114A-2	US-08-170-114A-2	US-08-660-092-70	US-09-160-513-70	-60-	US-09-042-107-219	US-09-722-250D-219	17	US-08-182-967-12	US-08-645-193B-3	5217869-110	US-08-866-545-24	US-09-428-082B-116	US-09-627-775-24	US-09-258-754-183	042	US-08-182-967-11	US-09-722-250D-183	US-07-732-114A-6	US-08-170-114A-6	US-08-645-193B-7	US-08-645-193B-59	-099-80-	US-08-660-092-151
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152, 150, 151, 152, 91, 344,	Sequence 35, Appl Sequence 1, Appli Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 1066, Ap	
US-08-660-092-152 US-09-160-513-150 US-09-160-513-151 US-08-160-513-152 US-08-250-789A-91 US-09-489-847-344 US-08-212-433A-30 US-08-212-433A-30 US-08-212-433A-30	US-09-069-877A-35 PCT-US95-01239-30 US-07-732-114A-1 US-08-110-114A-1 US-08-811-682-20 US-09-089-878-1 US-09-089-878-2 US-09-460-384-9 US-09-187-859-1066 US-09-839-542B-1066	
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ALIGNMENTS

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Sequence 63, Application US/09258754

Patent No. 6174687

GENERAL INFORMATION:
APPLICANT: Rucolabti, Erkki
APPLICANT: Rajotte, Daniel
ITILE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
ITILE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
ITILE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
ITILE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
ITILE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
ITILE OF INVENTION NUMBER: US/09/258,754

CURRENT FILING DATE: 1999-02-26

EARLIER FILING DATE: 1999-03-13

NUMBER OF SEQ ID NOS: 452

SEQ ID NOS: 452

SEQ ID NOS: 452

SEQ ID NOS: 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-258-754-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
RESULT 1
US-09-258-754-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGIH: 9
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Query Match 38.9%; Score 28; DB 3; Length 9; Best Local Similarity 71.4%; Pred. No. 3e+05; Matches 5; Conservative 1; Mismatches 1; Indels 7 KSTNTFC 13 à

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Gaps

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Sequence 63, Application US/09042107
Fatent No. 6232287
GENERAL INFORMATION:
The sequence of t :|||| | 3 RSTNTGC 9 RESULT 2 US-09-042-107-63 g

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US-08-170-114A-2
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APPLICANT: Ruoslahti, Erkki
APPLICANT: Ruoslahti, Erkki
APPLICANT: Ruoslahti, Erkki
APPLICANT: Ruoslahti, Renata
TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
TITLE OF INVENTION: Tissues
FILE REFERENCE: P-14 4514
CURRENT FILING DATE: 2000-11-22
PRIOR APPLICATION NUMBER: US 09/042,107
PRIOR APPLICATION NUMBER: US 09/042,107
PRIOR FILING DATE: 1998-03-13
NUMBER OF SO ID NOS: 437
SOFTWARE: PATENTIN VOF. 2.0
                                 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-042-107-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-722-250D-63
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38.9%; Score 28; DB 4; Length 9;
Best Local Similarity 71.4%; Pred. No. 3e+05;
Matches 5; Conservative 1; Mismatches 1; Indels
                                                                                                            Query Match 38.9%; Score 28; DB 3; Length 9; Best Local Similarity 71.4%; Pred. No. 3e+05; Matches 5; Conservative 1; Mismatches 1; Indels
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; Sequence 2 Application US/07732114A
; Patent No. 5298396
; Patent No. 5298396
; Patent No. 5298396
; APPLICANT: KOTZIN, BRIAN L.
; APPLICANT: KAPPLER, JOHN
; APPLICANT: KAPPLER, JOHN
; APPLICANT: KAPPLER, JOHN
; TITLE OF INVENTION: METHOD FOR IDENTIFYING T CELLS
; TITLE OF INVENTION: INVOLVED IN AUTOIMMUNE DISEASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIF: 80237
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage COMPUTER: IBM compatible OPERATING SYSTEM: MS-DOS SOFTWARE: WORDPETFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Beaton & Swanson, P.C.
4582 South Ulster Street Parkway, #403
                                                                                                                                                                                                                                                                                                                                                                   Sequence 63, Application US/09722250D Patent No. 6610651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 KSTNTFC 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: Colorado COUNTRY: USA
                                                                                                                                                                                                            7 KSTNTFC 13
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STREET: 458
                                                                                                                                                                                                                                                                                                                          RESULT 3
US-09-722-250D-63
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LENGTH: 9
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APPLICANT: MARRACK, PHILIPPA
APPLICANT: MARRACK, PHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER KEADAMALE FOATH,

MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB storage COMPUTER: IBM pc compatible OPERATING SYSTEM: MS-DOS SOFTWARE: WORDERFECT 6.0 (a) For Windows SOFTWARE: WORDERFECT 6.0 (a) For Windows APPLICATION DATA: APPLICATION DATA: 20-DECEMBER-1993 CLASSIFICATION: 435 PRIOR APPLICATION DATA: 20-DECEMBER-1993 FILING DATE: 18-JULY-1991 PRIOR APPLICATION NUMBER: 07/488,353 FILING DATE: 2-MARCH-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 27; DB 1; 1
Pred, No. 2.1e+02;
1; Mismatches 4;
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8400 E. Prentice Avenue, Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 2-MARCH-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07,437,370
FILING DATE: 15-NOVEMBER-1989
ATTORNEY/AGENT INFORMATION:
NAME: Ullie L. Betnard
REGISTRATION NUMBER: 36,450
REFERENCE/DOCKET NUMBER: NJH217.3
PILING DATE: 18-JULY-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/488,353
FILING DATE: 2-MARCH-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/437,370
FILING DATE: 15-NOVEMBER-1989
ATYONEY/AGENT INFORMATION:
NAME: BALTY J. SWANSON
REGISTRATION NUMBER: 33,215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 850-9900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (303) 850-9401
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 54.5
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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US-07-732-114A-2
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Sequence 70, Application US/09160513

Patent No. 6410775

GENERAL INFORMATION:
APPLICANT: Victoria, Edward J.
APPLICANT: Victoria, David M.
APPLICANT: Jones, David M.
APPLICANT: TV, Lin
ITLE OF INVENTION: apL IMMUNOREACTIVE PEPTIDES, CONJUGATES THEREOF AND METHODS ON WIMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSE: MORRISON & FORESTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 219, Application US/09258754
; Sequence 219, Application US/09258754
; Patent No. 6174687
; GENERAL INFORMATION:
; GENERAL INFORMATION:
; APPLICANT: Pasqualini, Erkki
; APPLICANT: Pasqualini, Renata
; APPLICANT: Rajotte, Daniel
; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
; TITLE OF INVENTION: Membrane Dipeptidase
; TITLE OF INVENTION: Membrane Dipeptidase
; FILE REFERENCE: P-LJ 3443
; CURRENT APPLICATION NUMBER: US/09/258,754
; CURRENT FILING DATE: 1998-03-13
; CURRENT FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 452
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 219
; LENGTH: 13
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                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/160,513
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Pred. No. 3e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: CATHERINE M. POLIZZI
REGISTRATION NUMBER: 40.130
REFERENCE/DOCKET NUMBER: 2523:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEPHONE: (650) 844-0792
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INPORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amin 27
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Best Local Similarity 71.4
Matches 5; Conservative
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: sir
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                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 94304-1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CASELGK
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THEREOF AND METHODS OF TREATMENT FOR APL ANTIBODY-MEDIATED
PATHOLOGIES
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                                                                                                                                                                                                             37.5%; Score 27; DB 1; Length 13; 54.5%; Pred. No. 2.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,092
FILING DATE: 06-JUN-1996
CLASSIFICATION: 435
ATTONNEY/AGENT INPOMMATION:
NAME: PARK, Freddie K
REGISTRATION NUMBER: 35,636
REFERENCE/DOCKET NUMBER: 35,636
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAK: (415) 813-5600
TELEFRAK: (415) 813-5600
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                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Victoria, Edward J.
APPLICANT: Victoria, Edward J.
APPLICANT: Victoria, David M.
APPLICANT: Jones, David M.
APPLICANT: Yu, Lin
TITLE OF INVENTION: APL IMMUNOREAC
TITLE OF INVENTION: PATHOLOGIES
NUMBER OF SEQUENCES: 216
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 70, Application US/08660092
Patent No. 6207160
               TELEPHONE: (303) 793-3333
TELEFAX: (303) 795-3433
INPORMATION POS SEQ ID NO: 2:
SEQUENCE CHARACTELSTICS:
LENGTH: 13 amino acids
TYPE: amino acid
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71.4%;
TELECOMMUNICATION INFORMATION:
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Best Local Similarity 71.4
Matches 5; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                          6; Conservative
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Best Local Similarity
Matches 6; Conserv
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US-08-660-092-70
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CASELGKSTNTFC 13
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LENGTH: 13
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Patent No. 6232287
GENERAL INFORMATION:
APPLICANT: Rucelahti, Erkki
APPLICANT: Pasqualini, Renata
TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
TITLE OF INVENTION: MOMBER: US/09/042,107
CURRENT FILING DATE: 1998-03-13
NUMBER OF SEQ ID NOS: 436
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 219
LENGTH: 13
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Patent No. 6610651

GENERAL INFORMATION:
APPLICANT: Ruoslahti, Erkki
APPLICANT: Pasqualini, Renata
TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
TITLE OF INVENTION: Missues
FILE REFERENCE: P-LJ 4514
CURRENT APPLICATION NUMBER: US/09/722,250D
CURRENT FILING DATE: 2000-11-22
PRIOR PLILING DATE: 1999-03-13
NUMBER OF SEQ ID NOS: 437
SOFTWARE: PatentIn Ver. 2.0
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                                           FEATURE:

CTHER INFORMATION: Description of Artificial Sequence: Synthetic

US-09-258-754-219
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                                                                                                                                        Query Match
36.1%; Score 26; DB 3; Length 13;
Best Local Similarity 30.8%; Pred, No. 3e+02;
Matches 4; Conservative 2; Mismatches 7; Indels
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Pred. No. 3e+02;
2; Mismatches 7; Indels
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TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 30.8%;
Matches 4; Conservative
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US-09-042-107-219
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LENGTH: 13
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APPLICANT: FEIGE, ULRICH
APPLICANT: ELIU, CHUAN-AS
APPLICANT: CHESTHAN JANET C.
APPLICANT: CHESTHAN JANET C.
APPLICANT: CHESTHAN JANET C.
APPLICANT: BOONE, THOMAS CHARLES
TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
FILE REFERENCE: A-527
CURRENT APPLICATION NUMBER: US/09/428,082B
CURRENT FILING DATE: 1999-10-22
PRIOR PRICH DATE: 1999-10-23
NUMBER OF SEQ ID NOS: 1133
SOFTWARE: PATENTIN VERSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Chang, Jennie C.C.
APPLICANT: Brostoff, Steven W.
APPLICANT: Carlo, Dennis J.
TITLE OF INVENTION: Peptides and Methods Against Psoriasis
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36.1%; Score 26; DB 4; Length 13; 100.0%; Pred. No. 3e+02; cive 0; Mismatches 0; Indels
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MEDIUM TYPE: RADAPY disk
MEDIUM TYPE: RADAPY disk
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
FILING DATE: 14-73N-1994
FILING APPLICATION NUMBER: US/08/182,967
FILING APPLICATION NUMBER: US 08/462,471
FILING DATE: 05-7UN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/813,867
FILING DATE: 14-DEC-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: CALMODULIN ANTAGONIST PEPTIDE US-09-428-082B-170
                                                                                                             US-09-428-082B-170
; Sequence 170, Application US/09428082B
; Patent No. 6660843
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; Patent No. 6413516
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
1 CGSHCGOLCKSLC 13
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Matches 4; Conservative
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Gaps
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APPLICANT: Greene, Mark I.
APPLICANT: Murali, Ramachandran
APPLICANT: Takasaki, Wataru
TITLE OF INVENTION: PEPTIDES AND PEPTIDE
TITLE OF INVENTION: NECROSIS PACTOR RECEPTOR SUPERFAMILY AND THEIR
TITLE OF INVENTION: USES
CORRESPONDENCES: 27
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                   1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
5217869-110
; Patent No. 5217869
; APPLICANT: KAUVAR, LAWRENCE M.
; APPLICANT: METHOD TO PRODUCE IMMUNODIAGNOSTIC
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 24; DB 6;
Pred. No. 3e+05;
                                                                                                                                                                                                                                                1; Mismatches
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STREET: 1155 Avenue of the Americas
CITY: NW York
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/255,906
FILING DATE: 11-OCT-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/866,545
FILING DATE: 30-MAY-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 24, Application US/08866545; Patent No. 6265535; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33.3%;
57.1%;
      INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                4; Conservative
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ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 GKSTNTF 12
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Best Local Similarity
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Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                     1 SFNSFC 6
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                                                                                                                                                            US-08-645-193B-3
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                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/08645193B
Patent No. 5562253
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Kupke, Thomas
APPLICANT: Kempter, Christoph
APPLICANT: Manger, Christoph
TITLE OF INVENTION: Oxidative Decarboxylation of Peptides
TITLE OF INVENTION: Catalyzed by Flavoprotein EpiD
NUMBER OF SEQUENCES:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Sterne, Kessler, Goldstein & Fox P.L.L.C.
1100 New York Avenue, Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:

MEDIUM TRYER: Floppy disk

MEDIUM TRYER: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/645,193B

FILING DATE: 13-MAY-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Esmond, Robert W.

REGISTRATION NUMBER: 32,893

REGISTRATION NUMBER: 32,893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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TELECOMMUTICATION:
TELEPHONE: (202) 371-2600
TELEPAX: (202) 371-2540
APPLICATION NUMBER: US 07/644,611
PRIOR APACE 22-JAW-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/530,229
FILING DATE: 30-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/382,085
FILING DATE: 18-JUL-1989
PRIOR APPLICATION NUMBER: US 07/382,086
FILING DATE: 18-JUL-1989
PRIOR APPLICATION NUMBER: US 07/326,314
FILING DATE: 18-JUL-1989
PRIOR APPLICATION NUMBER: US 07/326,314
FILING DATE: 21-MAR-1989
ATTORNEY, AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: 31,815
REFERENCE/DOCKET NUMBER: 9-IM 9830
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (619) 535-9001
TELEPAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 12:
SEQUIENCE CHARACTERISTICS:
LENGTH: 12 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 12 amino acids
amino acid
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Matches 7; Conserv
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US-08-645-193B-3
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Y protein - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: 137263
C;Accession: 137263
R;Waeber, G.; Habener, J.F.
Endocrinology 131, 2010-2015, 1992
A;Title: Novel testis germ cell-specific transcript of the CREB gene contains an alterna A;Reference number: 137263; MUID:93010691; PMID:1396344
A;Accession: 137263
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: Le cRES>
A;Cross-references: EMBL:X68994; NID:g396171; PIDN:CAA48780.1; PID:g579816
C;Genetics:
A;Genetics:
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protein D - Escher
mitosis inhibiting
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lipopeptide WS1279
calsequestrin, fas
metallothionein is
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vicilin 57K chain
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                                                                         5, 2004, 10:36:12; Search time 22 Seconds (without alignments) 34.979 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                       283366 seqs, 96191526 residues
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Maximum Match 100%
Listing first 45 summaries
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A12016
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C61512
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Gapop 10.0 , Gapext 0.5
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XEYDGD
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A32014
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Match Length DB
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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Maximum DB
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Gaps

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Score 17; DB 2; Length 6; Pred. No. 2.8e+05; 0; Mismatches 1; Indels

37.0%; milarity 75.0%; Conservative 0

30 31	10	21.7	99	01 01	S11556 S60293	hydrogensulfite re tubulin beta-3 cha
32	10	21.7	7	~	871870	
333	10	21.7		01 N	S08606 B33882	hypothetical prote cadmium-hinding he
35	10	21.7		1 (1	PT0529	T-cell receptor be
36	10	21.7	7	01	S45648	Na+-transporting A
37	10	21.7	7	α,	990608	globulin IV alpha
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υ d	0 6	24.7	n o	7 (15/U18	gene citr protein
4 4	10	21.7	0 00	4 (A01337 S29272	cycocherol-binding
4.2	10	21.7	σ (1 (7)	157532	dene Thislow prote
43	10	21.7	89	7	A25836	L-serine ammonia-1
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					ALIGNMENTS	
RESULT 1 S29637	‡ }				1	
C;Species: Artocarpus C;Date: 19-Mar-1997 #	Artoc	carpus ch	- Arcocarpus champeden equence revis	en rej	sion 24-Jul-1998 #text	change 24-Jul-1998
C; Accession: S29637	n: S2	9637				
R;Ngoc, L.D.; Brillard, M.; Hoebeke, J. Biochim. Biophys. Acta 1156, 219-222, 1993 A;Title: The alpha- and beta-subunits of the Apple o	D.; Bi Siophys The alg	rillard, s. Acta 1 pha- and per. S. Ser.	M.; Ho 156, 3 beta-8	219-	rd, M.; Hoebeke, J. tta 1156, 219-222, 1993 and beta-subunits of the jacalins are \$296335, MITH.0315-561, DMID.8472970	cleavage products from a 17-k
A,Accession: S29637	n: \$25	9637	100	1	0.00750:01H (10.07616)	
A;Molecule type: protein A;Residues: 1-6 <ngo></ngo>	type 1:6	: protein				
A, Experimental source: seed C. Complex: heterotetramer: two alpha	ental s heter	source: s	seed er: two	[a]	oha and two beta chains	
C; Function	, i	7				
A; Description: seed storage A; Note: lectin for D-galacto C; Keywords: heterotetramer;	ctin fir hete	seed stor for D-gal erotetram	age practos; er, le	protein syl-beta lectin;	#,ivescription: seed storage protein A;Note: lectin for D-galactosyl-beta-1->3-N-acetylgalactosamine C;Keywords: heterotetramer; lectin; seed; storage protein	samine
Query Match	tch	:	37.0%;	. k		ı 6;
Best Local Matches		Similarity 75. 3; Conservative	75.(ative	 %	Pred, No. 2.8e+05; 1; Mismatches 0; Inc	Indels 0; Gaps 0;
à	2 N	NEES 5				
Db	1 N	NEQS 4				
RESULT 2 137263	,	:				

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C;Species: Kluyvera cryocrescens
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C;Accession: 51928
R;Accession: 51928
R;Martin, J.; Slade, A.; Aitken, A.; Arche, R.; Virden, R.
Biochem. J. 280, 659-662, 1991
A;Title: Chemical modification of serine at the active site of penicillin acylase from K
A;Reference number: 519288; MUID:92109664; PMID:1764029
A;Accession: 519288
A;Atatus: preliminary
A;Molecule type: protein
A;Residues: 1-8 <MAR>
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C.Species: Kaiware daikon (Japanese radish)
C.Species: Kaiware daikon (Japanese radish)
C.Jacte: 10-Mar-1998 #sequence_revision 10-Mar-1998 #text_change 17-Apr-1998
C.Jaccession: S65165
R.Obata, S.; Nishimura, M.; Nagai, K.; Sakihama, N.; Shin, M.
Arch. Biochem. Biophys. 316, 797-802, 1995
A;Title: Four ferredoxins from Japanese radish leaves.
A;Reference number: S69164; MUID:95168867; PMID:7864635
A;Molecule type: protein
C.Keywords: 1-8 <a href="Psecult-ransfer">CSECTOR</a>
C;Keywords: 2Fe-2S; electron transfer; iron-sulfur protein
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32.6%; Score 15; DB 2; Length 8;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 1; Indels
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Similarity 100.0%; Pred. No. 2.8e+05; 2; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                  acylase - Kluyvera cryocrescens
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nes 2, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          calsequestrin, fast skeletal muscle - rabbit (fragment)
(Species: Oryctolagus cuniculus (domestic rabbit)
(Spacies: 23-Aug-1991 #sequence_revision 23-Aug-1991 #text_change 23-Feb-1997
(SAccession: B39040
R;Cala, S.E.; Jones, L.R.
J. Biol. Chem. 266, 391-398, 1991
A;Title: Phosphorylation of cardiac and skeletal muscle calsequestrin isoforms by casein A;Reference number: A39040; MUID:91093153; PMID:1985907
A;Accession: B39940
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C;Species: Streptomyces willmorei
C;Date: 20-Apr_2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
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A;Residues: 1-8 <BRRA
C;Superfamily: metallothionein
C;Keywords: chelation; metal binding; metal-thiolate cluster
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A,Molscule type: protein
A;Residues: 1-7 <CAL>
C;Keywords: phosphoprotein; skeletal muscle
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Best Local Similarity 100.0%;
Matches 2; Conservative 0
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Best Local Similarity 60.0
Matches 3; Conservative
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Cispecies: Escherichia coli plasmid R100 (fragment)
Cispecies: Escherichia coli
Cispecies: Escherichia coli
Cispecies: Escherichia coli
Cispecies: Escherichia coli
Cispecies: Schorloss | Sacquence_revision 22-Jun-1989 | #text_change 16-Feb-1997
Cispecies: Alonamoto, S.; Yoshioka, Y.; Ohtsubo, E.
J. Bacteriol. 170, 2749-2757, 1988
J. Bacteriol. 170, 2749-2757, 1988
J. Bacteriol. 170, 2749-2757, 1988
J. Reference number: A32014; MUD:88227859; PMID:2836369
A)Accession. A32014
A)Status: preliminary
A;Molecule type: DNA
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C.Sate: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 07-Feb-1997
C.Accession: H48394
R.Mather, I.H.; Banghart, L.R.; Lane, W.S.
Biochem, Mol. Biol. Int. 29, 545-554, 1993
A.Title: The major fat-globule membrane proteins, bovine components 15/16 and guinea-pig II-like sequences.
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                                                                                                                                               Gaps
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Pred. No. 2.8e+05;
1; Mismatches 0; Indels
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                                                                                         Score 14; DB 2; I
Pred. No. 2.8e+05;
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50.0%; Pred. No. 2.8e+05;
iive 1; Mismatches 1;
                                                                 30.4%; Scor.
40.0%; Pred. No. 2..
3, Mismatches
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Matches 2; Conservative 1
        A;Residues: 1-8 <FOL>
C;Keywords: phosphotransferase
                                                                                                            Best Local Similarity 40.0
Matches 2; Conservative
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Best Local Similarity
Matches 2; Conserv
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C; Keywords: DNA binding
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C;Genetics:
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                                                                                                                                                                                                                                                   Na+/K+exchanging ATPase (EC 3.6.3.9) alpha chain - dog (fragment)
Cispecies: Canis lupus familiaris (dog)
Cipate: 19-Mar-1997 #sequence_revision 24-Jul-1998 #text_change 19-Apr-2002
CiAccession: 829881
R'Walderhaug, M.O.; Post, R.L.; Saccomani, G.; Leonard, R.T.; Briskin, D.P.
J. Blol. Chem. 260, 3852-3859, 1985
A)Title: Structural relatedness of three ion-transport adenosine triphosphatases around
A,Reference number: 829881; MUID:85131201; PMID:3156136
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B.Follettie, M.T.; Peoples, O.P.; Agoropoulou, C.; Sinskey, A.J.

A.Title: Gene structure and expression of the Corynebacterium flavum N13 ask-asd operon.

A.Accession: B47594

A.Accession: B47594
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A;Residues: 1-6 <WAL>
A;Experimental source: kidney
C;Keywords: ATP; heterodimer; hydrolase; ion transport; osmoregulation; phosphoprotein;
F;4/Active site: Asp (aspartylphosphate intermediate) #status predicted
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C;Species: Cladobotryum dendroides
C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 31-Dec-1993
                                Gaps
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                                Indels
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Pred. No. 2.8e+05;
1; Mismatches 1;
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llarity 75.0%; Pred. No. 2.8e+05;
Conservative 0; Mismatches 1;
  60.08;
                           3; Conservative
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Fed. Proc. 31, 447, 1972
A; Reference number: A01341
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Best Local Similarity
---------------------------3; Conserv?
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2 CSDKT 6
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                     Matches
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B34818
C; Species: Cajanus cajan (pigeon pea)
C; Species: Cajanus cajan (pigeon pea)
C; Species: Cajanus cajan (pigeon pea)
C; Species: 13-011-1990 #sequence_revision 13-011-1990 #text_change 30-Sep-1993
C; Accession: B34818
E; Mawal, Y.R.; Mawal, M.R.; Ranjekar, P.K.
Biochem: Biophys. Res. Commun. 166, 1446-1452, 1990
A; Title: Unusual denaturation properties of vicilin from Cajanus cajan.
A; Reference number: A34818
A; Reference number: A34818
A; Reference preliminary
A; Molecule type: protein
A; Molecule type: protein
A; Residues: 1-7 < MAW>
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A;Accession: H48394
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-6 <MAT>
A;Resperimental source: milk
A;Note: sequence extracted from NCBI backbone (NCBIP:131518)
C;Keywords: glycoprotein
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Search completed: September 5, 2004, 10:40:20 Job time : 23 secs

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MEDLINE=88227859; PubMed=2836369; Inamoto S., Yoshioka Y., Ohtsubo E.; Inamoto S., Yoshioka Y., Ohtsubo E.; "Identification and characerization of the products from the traJ and traY genes of plasmid R100."; J. Bacteriol. 170:2749-2757(1988).
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(c) 1993 - 2004 Compugen Ltd.
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Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
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ses 2; Conservative
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                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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    -I- FUNCTION: May play a structural role in the elaioplast, a tapetum-
specific plastidial lipid organelle.
    -!- TISSUE SPECIFICITY: Tapetum of anthers.

                                                                                                                                                                                                                                                                                                                                                                                                                                         Brassica napus (Rape).

Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Brassica.
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PROCESS OF BACTERIAL CELLS FOR THE EXCHANGE OF PLASMID DNA.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to the tram family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0CT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Uhknown protein from 2D-page of fibroblasts (Fragment).
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hernandez-Pinzon I., Ross J.H.E., Barnes K.A., Damant A.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
28.3%; Score 13; DB 1; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                  Length 5;
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                                                                                                                                                                                                        5 AA; 634 MW; 6B1B1AA443500000 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                 15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Plastidial lipid-associated protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                          8 AA.
                                                                                                                                                      EMBL; M20941; -; NOT_ANNOTATED_CDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE.
STRAIN=CV. TOPAZ; TISSUE=Tapetum;
MEDLINE=99349136; PubMed=10420651;
                                                                                                                                                               PIR; A32014; A32014.
Conjugation; Plasmid; DNA-binding.
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es 2; Conserv
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P38641;
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P81707;
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ID UF03 MC
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                                                                                                                                                     MEDLINE=95009907; PubMed=7523108; MEDLINE=95009907; PubMed=7523108; Merzinck B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.; Separation and sequencing of familiar and novel murine proteins using preparative two-dimensional gel electrophoresis."; Electrophoresis 15:735-745(1994).

-!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown protein is: 5.1, its MW is: 36 kDa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Plasma protein map: an update by microsequencing.";
Electrophoresis 13.707-714 (1992).
-!- MISCELLANBOUS: On the 2D-gel the determined pI of this unknown protein is: 4.9, its MW is: 65 kDa.
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-APR-1993 (Rel. 25, Last sequence update)
115-MAR-2004 (Rel. 43, Last annotation update)
Unknown protein from 2D-page of plasma (Spot 2) (Fragment).
Homo sapiens (Hunan).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26.1%; Score 12; DB 1; Length 8; 50.0%; Pred. No. 1.40+05; tive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hughes G.J., Frutiger S., Paguet N., Ravier F., Pasquali
Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
Hochstrasser D.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    7 AA; 842 MW; 6AA72B1DDB1B1180 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 Similarity 50.0%; Pred. No. 1.4e+05; 2; Conservative 2; Mismatches 0
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Bromoheptapeptide Im.
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in all eukaryotic cells.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN IS:
                                                                                                                                                                                                                        Sex pheromone CAD1.
Enterococcus faecalis (Streptococcus faecalis).
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
NCBI_TaxID=1351;
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE.
MEDLINE=85051889; PubMed=6437872;
MOTI M., Sagakami Y., Narita M., Isogai A., Fujino M., Kitada C.,
Craig R.A., Clewell D.B., Suzuki A.;
"Isolation and structure of the bacterial sex pheromone, cADI, that
induces plasmid transfer in Streptococcus faecalis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEBS Lett. 178:97-100(1984).
-!- FUNCTION: CAD1 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE
HEMOLYSIN PLASMID PAD1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "A transaldolase. An enzyme implicated in crab steroidogenesis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lachaise F., Somme G., Carpentier G., Granjeon E., Webster S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Carcinus maenas (Common shore crab) (Green crab).

Bukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;

Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;

Bubrachyura; Portunoidea; Portunidae; Carcinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOILING 7.23-24(1990).
FUNCTION: Actions are highly conserved proteins that are in various types of cell motility and are ubiquitously
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 11; DB 1; Length 8; Pred. No. 1.4e+05; 1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 AA; 819 MW; 047DD732C735B9C7 CRC64;
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01-0CT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                   (Rel. 13, Last sequence update) (Rel. 17, Last annotation update)
                                                                                                          8 AA.
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-!- SIMILARITY: Belongs to the actin family.
InterPro; IPR004001; Actin.
InterPro; IPR004000; Actin.like.
PROSITE; PS00406; ACTINS 1; PARTIAL.
PROSITE; PS00432; ACTINS 2; PARTIAL.
PROSITE; PS01132; ACTINS_ACT_LIKE; PARTIAL.
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                                                                                                          PRT;
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                                                                                                                                                         01-JAN-1990 (Rel. 13, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23.9%;
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                                                                                                          STANDARD;
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NON_TER 1
NON_TER 8
SEQUENCE 8 AA; 976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Baghdassarian D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Actin (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 SLI 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 SLV 5
                                                                                                                                                                                                           01-FEB-1991
                                                                                                        CAD1 ENTFA
P13268;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACT CARMA
P80709;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pheromone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SECUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                   CAD1_ENTFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACT_CARMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 9
                                                         RESULT
                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neuron 2:1465-1473(1989).
-!- FUNCTION: Potent modulator of inhibitory motorneurons. Reduces the input resistance and blocks slow oscillatory potentials in these
                                                                                                                                                                                                                                               "A novel post-translational modification involving bromination of tryptophan. Identification of the residue, L-6-bromotryptophan, in peptides from imperialis and Conus radiatus venom.";
J. Biol. Chem. 272:4689-469811997).
-!- FUNCTION: Does not elicit gross behavioral symptoms when injected centrally or peripherally in mice.
-!- SUBCELLUIAR LOCATION: Secreted.
-!- SUBCELLUIAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Expressed by the venom duct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FMRFamide-like neuropeptide AFI.
Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
Bukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea; Ascarididae; Ascaris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=90180465; PubMed=2627377;
Cowden C., Stretton A.O.W., Davis R.E.;
"AFI, a sequenced bioactive neuropeptide isolated from the nematode
Ascaris suum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- TISSUE SPECIFICITY: Found in the nerve cords and a variety of
                                                                                                                                                                         Craig A.G., Jimenez E.C., Dykert J., Nielsen D.B., Gulyas J.,
Abogadie F.C., Porter J., Rivier J.E., Cruz L.J., Olivera B.M.,
McIntosh J.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda; Neogastropoda; Conoidea; Conidae; Conus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ganglia particularly in the anterior regions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .,0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 11; DB 1; Length 7;
Pred. No. 1.4e+05;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PYRROLIDONE CARBOXYLIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; ASB512; ASB512.
Bromination; Amidation; Pyrrolidone carboxylic acid. DISULED. 2. 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6EA37DC6D87EA6B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 AA; 953 MW; 69D40059CB144350 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23.9%; Score 11; DB 1; Le 100.0%; Pred. No. 1.4e+05; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-001-1993 (Rel. 26, Created)
01-00L-1993 (Rel. 26, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 AA.
                                                                                                   SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BROMINATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AMIDATION
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                                                                                                                       TISSUE=Venom;
MEDLINE=97184108; PubMed=9030520;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 AA; 795 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neuropeptide; Amidation.
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es 2; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 1; Conserv
                                                    NCBI_TaxID=35631;
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AC P11889;
DT 01-07L-1993
DT 01-7UL-1993
DT 01-7UL-1993
DT 01-FEB-1996
DE RRFAMIGG-1996
OC BUKATYOTA;
OC BUKATYOTA;
NCBI TAXID=6
RX MEDLINE=9018
RY MEDLINE=9018
RA COWGEN C., S
RY "ARL, a SEQUENCE
RX MEDLINE=9018
RY ASCATIS SEQUENCE
C -1- FUNCTION
CC input re
CC cills.
CC -1- SIMILARIS
CC -1- SIMILAR
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MOD_RES
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Lote C.J., Weiss J.B.;

"Identification in urine of a low-molecular-weight highly polar
glycopptide containing cysteinyl-galactose.";

Biochem. J. 123:25P-25P(1917)

-!- FUNCTION: The identity of the glycoprotein from which this peptide
is derived is unknown. No physiological function has been
attributed. An erythrocyte membrane glycopeptide having a
similar structure has also been found.

PIR; A03188; XGHUEU.

GO; GO:0005576; C:extracellular; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Muscle;

WabinNe=25222120; PubMed=1807161;
Krishna R.G., Chin C.C.G., Wold F.;
"N-terminal sequence analysis of N alpha-acetylated proteins after
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
11-MAX-2004 (Rel. 44, Last annotation update)
Acylamino-acid-releasing enzyme (EC 3.4.19.1) (AARE) (Acyl-peptide hydrolase) (APH) (Acylaminoacyl-peptidase) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
NCBI_TaxID=9986;
                                                                                                                                                                                                                                              1.4e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19.6%; Score 9; DB 1; Length 8; 100.0%; Pred. No. 1.4e+05; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                           Length
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8 AA; 855 MW; C2D87AA1F5B1EB1E CRC64;
                                                                                                      4 4 D-LEUCINE.
8 AA; 890 MW; 75A367672732CEB8 CRC64;
-!- SIMILARITY: Belongs to the contryphan family.
Toxin; Hydroxylation; D-amino acid.
DISULEID 2 8 D-LEUCINE.
                                                                                                                                                                                                                           DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 AA.
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                                                                                                                                                                                                                       19.6%; Score 9; DB 1
100.0%; Pred. No. 1.4
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=72062338; PubMed=5126885;
                                                                                                                                                                                                                                                             Local Similarity 100.
nes 1; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Urine glycopeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glycoprotein.
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P25154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GLUR HUMAN
P02729;
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                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLUR_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACPH RABIT
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last sequence update)
10-FEB-1996 (Rel. 33, Last annotation update)
11-FEB-1996 (Rel. 33, Last annotation update)
12-FEB-1996 (Rel. 33, Last annotation update)
13-FEB-1996 (Rel. 33, Last annotation update)
13-FEB-1996 (Rel. 31, Last annotation update)
14-FEB-1996 (Rel. 31, Last annotation update)
15-FEB-1996 (Rel. 31, Last annotation update)
16-FEB-1996 (Rel. 31, Last annotation update)
17-FEB-1996 (Rel. 31, Last annotation update)
18-FEB-1996 (Rel. 31, Last annotation upd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Sarcophaga) bullata.";
Regul. Pept. 50.61-72(1994).
-!- FUNCTION: Has an oostatic activity. Inhibits trypsin biosynthesis in the midgut which indirectly reduces the vitallogenin concentration in the hemolymph resulting in inhibition of oocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jacobsen R.B., Jimenez E.C., De la Cruz R.G.C., Gray W.R., Cruz L.J.,
           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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J. Pept. Res. 54:33-99(1999).
-:- SUBCELLULAR LOCATION: Serveted.
-:- TISSUB SPECIFICITY: Expressed by the venom duct.
-:- MASS SPECTROMETRY: MW=888.4; METHOD=LSIMS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Sequencing and characterization of trypsin modulating oostatic factor (TMOF) from the ovaries of the grey fleshfly, Neobellieria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- DEVELOPMENTAL STAGE: Synthesized and released from follicular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bylemans D., Borovsky D., Hunt D.F., Shabanowitz J., Grauwels L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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Bukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19.6%; Score 9; DB 1; Length 6; 40.0%; Pred. No. 1.4e+05; Live 1; Mismatches 2; Indels
           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 AA; 695 MW; 61E72451B7642000 CRC64;
           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28.FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 AA.
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SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
STRAIN=Clipperton Island; TISSUE=Venom;
MEDLINE=99388839; PubMed=10461743
           1; Mismatches
                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         epithelium after a blood meal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=94211930; PubMed=8159807;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
           1; Conservative
                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE, AND SYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
les 2; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 NPTNL 5
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CN 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Ovary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             de Loof A.;
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TMOF SARBU
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COW2_CONPU

RESULT 11

Best Loc Matches

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Gaps

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                              Anal. Biochem. 199:45-50(1991).

-!- FUNCTION: This enzyme catalyzes the hydrolysis of the N-terminal peptide bond of an N-acetylated peptide to generate an N-acetylated amino acid and a peptide with a free N-terminus. It preferentially cleaves off Ac-Ala, Ac-Met and Ac-Ser.

-!- CATALYTIC ACTIVITY: Acylaminoacyl-peptide + H(2)O = acylamino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sex pheromone CCF10.

Enterococcus faecalis (Streptococcus faecalis).

Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.

(1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=CB1;

MEDLINE_2132712; PubMed=11429463;

De Angelis M., Bini L., Pallini V., Cocconcelli P.S., Gobbetti M.;

The acid-stress response in Lactobacillus sanfranciscensis CB1.";

"The acid-stress response in Lactobacillus sanfranciscensis CB1.";

"The Angelis M. 1:1863-1873 (2001).

-!- INDUCTION: Overexpressed in acid environments.

NON_TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco).
Bacteria, Firmicutes, Lactobacillales, Lactobacillaceae;
Lactobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 6;
1.4e+05;
ches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
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   unblocking with N-acylaminoacyl-peptide hydrolase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 AA; 775 MW; 6732D6C40B16F000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 AA; 778 MW; 6AA45B5B132A8000 CRC64;
                                                                                                                                                                                                                                                                                  -!- VUBUNIT: Homotetramer.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to peptidase family S9C.
PIR, 449792; A49792.
MEROPS; S09.004; -.
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01-FEB-1991 (Rel. 17, Last sequence update)
01-FEB-1991 (Rel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro, IPR002471; Pept S9 AS.
PROSITE; PS00708; PRO ENDOPEP SER; PARTIAL.
Hydrolase; Acetylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 8; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 8;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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50.0%;
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20.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Rel. 40, (Rel. 40,
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Best Local Similarity
Matches 1; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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ERQVL 6
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CCF1_ENTFA
AC CCF1_614;
DT 01-FEB-1991
DT 01-FEB-1991
DF Sex pheromon
OS Enterococus
OC Bacteria; Fi
OX NCB1_TaxID=1
RN [1]
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SEQUENCE.
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ASP2_LACSN
AD ASP2_LACSN
AD 16-0CT-
DT 16-0CT-
DT 16-0CT-
DE ACID SI
OC BACTEN
OC STRAIN
RR MEDLINN
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REPRESENTATION OF THE PROPERTY AND THE P
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RX MEDINE=89008313; PubMed=3139658;
RA Mori M., Sakagami Y., Ishii Y., Isogai A., Kitada C., Fujino M.,
RA Mori M., Sakagami Y., Ishii Y., Isogai A., Kitada C., Fujino M.,
RA Adsit J.C., Dunny G.M., Suzuki A.;
RT Adsit J.C., Dunny G.M., Specials ex pheromone which induces
RT conjugative transfer of the Streptococcus faecalis tetracycline
RT resistance plasmid, pCF10.";
RT Tesistance plasmid, pCF10.";
CC -!- FUNCTION: CCF10 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE
CC -!- FUNCTION: CCF10 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE
CC HEWOLYSIN PLASMID PCF10.
CC HEMOLYSIN P
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equus cabal
rousettus l
hylobates c
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pteropus gi
trichechus
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choloepus d
callimico g
                                                                                                         panthera on
didelphis m
                                          procavia ca
sorex arane
                                                          erinaceus c
                                                                  myrmecophag
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                          macaca mula
                                   loxodonta a
                 chaetophrac
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tamandua te
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                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Dioscoreales; Dioscoreacea;
Dioscorea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                       STRAINE-DT17-1;
MEDLINE-2027921; PubMed=10821191;
Terauchi R., Kahl G.
"Rapid isolation of promoter sequences by TAIL-PCR: the 5'-flanking regions of Pal and Pgi genes from yams (Dioscorea).";
MMOI. Gen. Genet. 263:554-560(2000).
EMBL; AB016716; BAA32235.1; --
GO; GO:0016853; F:isomerase activity; IEA.
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03bfb0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 18; DB 10; Length 8; Pred. No. 1e+06;
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                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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8 AA; 839 MW; F7BOS731BSA1ADD6 CRC64;
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                                                                                                                                                                                                                                                          ALIGNMENTS
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last seq
                               09BFA8
09BFB2
09BFB2
09BFB5
09BFB6
09BFB3
                                                                                                                                                                                                                                                                                                                                          Phosphoglucose isomerase (Fragment)
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Q9BF99
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Q9BF85
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Q9BFA4
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Q9BFB7
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Q9BFB4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 3; Conserv
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Dioscorea tokoro.
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Isomerase.
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Best Local
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Q67113
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Q67113 influenzavi
Q42564 fugu rubrip
Q8iv87 homo sapien
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03550 escherichia
09252 buchnera ap
09522 buchnera ap
09595 homo sapien
015895 homo sapien
015896 homo sapien
0962 macropus eu
09650 rragelaphus
09661 crinops te
096193 megapiera n
09631 ateles fusc
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                                                    5, 2004, 10:35:32; Search time 57 Seconds (without alignments) 44.283 Million cell updates/sec
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      GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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032560
Q9ZEZ9
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Gapop 10.0 , Gapext 0.5
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1: sp_archea:*
2: sp_bacteria:*
4: sp_fungi:*
5: sp_innean:*
6: sp_innextebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
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sp_unclassified:*
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sp_bacteriap:*
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STRAIN=Sprague-Dawley,
MEDLINE=96198747; PubMed=8612486;
Yoshikawa T., Makino S., Gao X.M., Xing G.Q., Chuang D.M.,
Detera-Wadleigh S.D.;
"Splice variants of rat TR4 orphan receptor: differential expression of novel sequences in the 5'-untranslated region and C-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                        Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DJ107712.2 (Serine palmitoyltransferase, long chain base subunit
2-like (Aminotransferase 2), variant 1) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yoshikawa T., DuPont B.R., Leach R.J., Detera-Wadleigh S.D., "New variants of the human and rat nuclear hormone receptor, expression and chromosomal localization of the human gene."; Genomics 35:361-366(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 28.3%; Score 13; DB 11; Length 7; Local Similarity 100.0%; Pred. No. 1e+06; es 2; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                      Smith M.;
Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AL050320; CAD54807.1; -
GO; GO:0016740; F:transferase activity; IEA.
                                                                                                                                                                                                                                                                                                                                Query Match 30.4%; Score 14; DB 4; Length 8; Best Local Similarity 66.7%; Pred. No. 1e+06; Matches 2; Conservative 1; Mismatches 0; Indels
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01-UUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                  NON_TER 1 1 SEGUENCE 8 AA; 908 MW; 8E533682CEBEB042 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 AA; 663 MW; 6DDAA8787EB05350 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0004872; F:receptor activity; IEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Sprague-Dawley;
MEDLINE=96299786; PubMed=8661150;
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Bukaryota, Metazoa, Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Takifugu.
                     01-NOV-1996 (TEMBLrel. 01, Created)
01-NOV-1996 (TEMBLrel. 01, Last sequence update)
01-CCT-2002 (TEMBLrel. 22, Last annotation update)
Influenza virus type A (Udorn/72) hemagglutinin (Seg 4) cDNA, 3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Truncated voltage-gated sodium channel alpha subunit (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                      Score 16; DB 12; Length 7;
Pred. No. 1e+06;
0; Mismatches 0; Indels
                                                                                               (Fragment).
Influenzavirus A.
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 1 7 AA; 730 MW; 75B72EA2C73772A0 CRC64;
                                                                                                                                                                                                                                                                                                                                                       7 AA; 834 MW; 605EB0544EA40030 CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
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NON TER 1 1 1
SEQUENCE 7 AA; 834 MW; FA
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50.0%;
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Best Local Similarity 50.0°
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                                                                                                                                                                                                                                                                                                 21:495-500(1980)
                                                                                                                                                   Influenza A viruses.
NCBI_TaxID=197911;
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SEQUENCE
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Q8IV87;
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RESULT 4 Q8IV87

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RESULT 6

032560 AC 032560 O3 DT 011 DT 011 DT 011 DT 011 DT 011 DE PT 011 DE P

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TISSUB=Placenta;
Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay B.A., Zhao Z.-Y.,
                                                                                                                                                                                                                                                                                                                                  "Molecular phylogenetics and the origins of placental mammals.";
Mature 409:614-618(2001).

BMBL: AYON1664; AAG47575.1; -
GO, GO:0005634; C:nucleus; NAS.
GO; GO:0005637; F:DNA binding; NAS.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; NAS.
SEQUENCE 8 AA; 1006 MW; DF02C331EEAB572A CRC64;
                                                                                                                                                                        Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Isolation of chromosome-specific genes by reciprocal probing of arrayed cDNAs and cosmid libraries.";

Hum. Mol. Genet. 0:0-0(1995).

EMBL; L32075; AAA73885.1; -.

NON TER 8

NON_TER 8
                                                                                                                                                                                                                                                                                   MEDLINE=21082082; PubMed=11214319;
Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
O'Brien S.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26.1%; Score 12; DB 4; Length 8; 66.7%; Pred. No. 1e+06;
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                                                                                01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
cAMP responsive element moderator (Fragment).
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
(Clone XP6A10A) (Fragment).
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Best Local Similarity
Matches 2; Conserv
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KSLV 8
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Q15895;
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                                                                                                                                                                                                                                                                        Hesslinger C., Sawers G.,
"The tdcE gene in Escherichia coli W3110 is separated from the rest of
the tdc operon by insertion of IS5 elements.";
DNA Seq. 9.183-188(1988).
EMBL, AJ001620; CAA04875.1; ...
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                                                                                                                                              Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NCBI_TaxID=562;
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actoria, Proteobacteria, Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Buchnera.
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SEQUENCE FROM N.A.
SIDJINE=99028904; PubMed=9812361;
Silva F.J., Van Ham R.C.H.J., Sabater B., Latorre A.;
Silva F.J., Van dea evolution of the leucine plasmids carried by the endosymbiont (Buchnera aphidicola) from aphids of the family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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Hers Microbiol. Lett. 168,3-49(1998).

EMBL; AJ006874; CAA77290.1;

GO; GO:0046821; C:extrachromosomal DNA; IEA.

GO; O:0003852; F:2:sopropylmalate synthase activity; IEA.

GO: GO:0016829; F:lyase activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      28.3%; Score 13; DB 2; Length 8; 100.0%; Pred. No. 1e+06; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26.1%; Score 12; DB 2; Length 8; 33.3%; Pred. No. 1e+06; ative 2; Mismatches 2; Indels
                                     01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
2-isopropylmalate synthase (EC 4.1.3.12) (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                           1 1
8 AA; 1000 MW; 3A505EB044140DC4 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 AA.
         PRT;
                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-W3110;
MEDLINE=99449059; PubMed=10520749;
                                                                                             Propionate kinase (Fragment)
       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Buchnera aphidicola.
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                                                                                                                               Escherichia coli
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032560
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RESULT 10 015890

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Tragelaphus eurycerus (Bongo).
Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Cetartiodactyla; Ruminantia, Pecora; Bovoidea;
Bovidae, Bovinae, Tragelaphus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Echinops telfairi (Lesser hedgehog tenrec).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                   Macropus eugenii (Tammar wallaby).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Metatheria, Diprotodontia, Macropodidae, Macropus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Molecular phylogenetics and the origins of placental mammals.";
Nature 409:614-618(2001).
Babli, Ax011673; Ax647583.1; -.
NON TEX
SEQÜENCE 8 AA; 978 MW; DF1DD331EEAB572A CRC64;
                                                                                                                                                                                                                                  "Molecular phylogenetics and the origins of placental mammals.";
Nature 409:614-618(2001).
EMBL; AY011621; AAG47536.1; -.
                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=21082082; PubMed=11214319;
Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A., O'Brien S.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINEs-21082082; PubMed=11214319;
Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A., O'Brien S.J.;
                                                                                                                                                                                                                                                                                                                                                                               1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26.1%; Score 12; DB 6; Length 8; 66.7%; Pred. No. 1e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
cAMP responsive element moderator (Fragment).
01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) cAMP responsive element moderator (Fragment).
                                                                                                                                                                                                                                                                                                          SEQUENCE 8 AA; 978 MW; DF1DD331EEAB572A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cAMP responsive element moderator (Fragment) CREM.
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es 2; Conservative
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                                                                                                                         NCBI_TaxID=9315;
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Q9BF90
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                                                            CREM
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                                                                                                                                                                                                                                                                        Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M., Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay B.A., Zhao Z.-Y.
                                                                                                                                                    Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Cornivora, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Ursidae, Ursus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Molecular phylogenetics and the origins of placental mammals."; Nature 409:614-618(2001).
EMBL; AY011683; AAG47591.1; -.
                                                                                                                                                                                                                                                                                                            Caskey C.T.H.;
Tablation of thromosome-specific genes by reciprocal probing of arrayed CDNAs and cosmid libraries.";
Hum. Nol. Genet. 0:0-0 (1995).
EMBL; L32083; AAA/3880.1; -.
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MEDLINES-21082082; PubMed=11214319;
Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A., O'Erien S.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26.1%; Score 12; DB 6; Length 8; illarity 66.7%; Pred. No. 1e+06; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                            01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                         B AA; 975 MW; 605EA6C5BEA5A2D3 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cAMP responsive element moderator (Fragment).
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                                             ₽
AA.
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01-JUN-2001 (TrEMBLrel. 17, Created)
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01-JUN-2001 (TrEMBLrel. 17, Last seq
01-JUN-2001 (TrEMBLrel. 17, Last ann
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                                             PRT;
                                                                                                                                   Clone XP19G12A) (Fragment).
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Best Local Similarity 33.5.
Local 1; Conservative
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                                           PRELIMINARY;
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Les 2; Conserv
                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
TISSUE=Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9644;
                                                                                                                                                                                                      NCBI_TaxID=9606;
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Q9BFC2
ID Q9BFC2
                                           Q15890
Q15890;
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      Mammalia; Butheria; Insectivora; Tenrecidae; Tenrecinae; Echinops.
VCBI_TaxID=9371;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Cetacea; Mysticeti;
Balaenopteridae; Megaptera.
                                                                                                                                                                   SEQUENCE FROM N.A.

MEDLINE=21082082; PubMed=11214319;

Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
O'Brien S.J.;
"Molecular phylogenetics and the origins of placental mammals.";
Mature 409:614-618(2001).

EMBL, AXV11632; AAG47547.1; -.

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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-21082082; PubMed=11214319;
Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
O'Brien S.J.;
"Molecular phylogenetics and the origins of placental mammals.";
Mature 409:614-618(2001).
EMBL; AXV11669; AAG47580.1; -.
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Pred. No. 1e+06;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9BF93;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CAMP responsive element moderator (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE 8 AA, 978 MW; DF1DD331EEAB572A CRC64;
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Best Local Similarity 66.7%;
Matches 2; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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Matches 2; Conserv
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29BF93
AC 29BF9
AC 29BF9
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DT 01-JU
DT 01-JU
DE CAMP
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

September Run on:

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US-09-761-636A-6 Perfect score:

1 CNEESLIC 8 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1586107 seqs, 282547505 residues Searched:

122046 Total number of hits satisfying chosen parameters:

seg length: 0 seg length: 8 Minimum DB : Maximum DB :

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

A_Geneseq_29Jan04:* 1: genesemine

geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* geneseqp2002s:* geneseqp2003as:* genesegp2003bs:* geneseqp2001s:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004s:*

SUMMARIES

Description	Aau04525 VEGF base	VEGF	VEGE	VEGF			Aay54526 Human CD4	_	Aar73350 Human TSH	Feline		Aar80365 Protein p		Aay48644 Membrane			Aaw25915 Beta-2-mi	Aar73349 Human TSH	Aar73348 Human TSH	Aaw12848 RGD-bindi	Aay48852 Membrane	Aay48662 Membrane	Aav48640 Membrane	Aabo6526 Claudin-2	Aabl7353 Integrin-
ΩI	AAU04525	AAU04539	AAU04541	AAU04538	AAU04540	AAR24954	AAY54526	AAR73351	AAR73350	AAY57040	AAU08451	AAR80365	AAW49750	AAY48644	ABG35021	AAU08460	AAW25915	AAR73349	AAR73348	AAW12848	AAY48852	AAY48662	AAY48640	AAB06526	AAB17353
DB	4	4	4	4	4	~	m	7	~	m	4	~	7	N	S	4	~	7	~	7	~	7	7	٣	٣
% Query Match Length	60	80	80	80	80	60	80	8	œ	80	6 0	ω	80	00	۵	6 0	7	60	8	80	80	8	80	80	89
% Query Match	100.0	93.5	91.3	89.1	84.8	S.	65.2	56.5	56.5	56.5	9	54.3	54.3	54.3	54.3	52.2	50.0	50.0	50.0	ö	。	。		50.0	50.0
Score	46	43	42	41	39	30	30		26	26	26	25	25	25	25	24	23	23	23	23	23	23	23	23	23
Result No.	1	73	m	4	ഗ	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

	Adeosi/s Febride # Abd34995 Human pro			Abb72952 Integrin	Aar93979 Partial p	Aay64349 Cadherin-	Aay64350 Cadherin-	Aaw70546 Peptide 1	Aay48874 Membrane		Aay48670 Membrane	Aay61125 Cadherin-	Aay64310 Cadherin-	_	Aay64348 Cadherin-		Aay62590 T-cadheri	
AAE08176	ABG34995	ABG34987	AAU81097	ABB72952	AAR93979	AAY64349	AAY64350	AAW70546	AAY48874	AAY48637	AAY48670	AAY61125	AAY64310	ABJ04389	AAY64348	AAM52891	AAY62590	AAY61019
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∞ ο	0 00	80	8	80	9	9	7	80	80	80	80	80	80	80	S	5	9	9
0.00	20.0	20.0	50.0	50.0	47.8	47.8	47.8	47.8	47.8	47.8	8	47.8	47.8	47.8	. 7	45.7		. 7
25.0	20	50	20	20	47	47	47	4	47	47	47	47	47	47	45.7	45	45	45
23	23	23	23	23	22	22	22	22	22	22		22	22	22	21	21	21	21
26	28 28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

AL I GNMENTS

RESULT

vascular endothelial growth factor; angiogenesis; neovascularisation, lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic. AAU04525 standard; peptide; 8 AA. VEGF based monocyclic peptide 2. (first entry) Human; VEGF; 26-SEP-2001 AAU04525; AAU04525

Synthetic

1..8 /note= "This bond cyclises the peptide" Location/Qualifiers Key Disulfide-bond

WO200152875-A1

26-JUL-2001.

18-JAN-2001; 2001WO-US001533.

18-JAN-2000; 2000US-0176293P. 16-MAY-2000; 2000US-0204590P.

(LUDW-) LUDWIG INST CANCER RES.

Cendron A; Stacker S, Hughes RA, Achen MG,

WPI; 2001-442248/47.

Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine residues

Claim 49; Page 32; 102pp; English.

The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human VEGFD (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring betabeta carbon separation distances on opposite antiparallel strands of a

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peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides) and a cyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with angiogenesis,

To cyclisation are used to interfere with angiogenesis,

Characterised by angiogenesis, newsscularisation or lymphangiogenesis.

The condition is diabetic retinopathy, psoriasis, arthropathy,

Cerebrovascular accident, post-angioplasty restenosis, head, heat or cold trauma, substance-induced neovascularisation of the liver, excessive cerebrovascular accident, post-angioplasty restenosis, head, heat or claimed, hypertension induced neovascular sequelae, hypertension induced neovascular sequelae, hypertension induced neovascular sequelae, hypertension induced neovascular permeability in a mammal (the mammal has a condition characterised by fluid accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain. The peptides are used to induced blood vessels and lymphatic or brain. The peptides are used to induce by VEGF. Or D and are also used in combination with an anti-inflammatory agent, to treat a continual accident inflammatory agent, to treat a continual accident inflammatory agent, to treat a continual accident activity induced by VEGF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neovascularisation, lymphangiogenesis; psoriasis; tumour;
diabetes induced neovascular sequelae; rheumatoid arthritis;
diabetic retinopathy; chronic inflammation; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 8;
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    .8
/note= "This bond cyclises the peptide"

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100.0%; Pred. No. 1.4e+06;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU04539 standard; peptide; 8 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                   diabetic retinopathy
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es 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8 AA;
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The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human whose 3-dimensional structure is modelled on the expose loop of human CV USCFD (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring beta-control of peptide by a measuring beta-control of peptide by oxidising the cysteine residues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior corplication are used to interfere with angiogenesis, coryclisation are used to interfere with angiogenesis, coryclication or lymphangiogenesis.

The condition is diabetic retinopathy, pooriasis, arthropathy, correctorised by angiogenesis, neovascularisation or lymphangiogenesis. The condition is diabetic retinopathy, pooriasis, arthropathy, correctorised by angiogenesis, neovascularisation or lymphangiogenesis. The condition is diabetic retinopathy, pooriasis, arthropathy, correctorised by angiogenic dysfunction, diabetes induced neovascular sequelae, hypertension induced neovascular sequelae, or chronic liver infection. The peptides are also used to modulate vascular permeability cor brain. The peptides are used to image blood vessels and lymphatic arc used to image blood vessels and lymphatic with at least one biological activity induced by VBGF, very and are also used in combination with an anti-inflammatory agent, to treat a correction inflammation, with an anti-inflammatory agent, to treat a corporation of periods.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  neovascularisation; lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 43; DB 4; Length 8; Pred. No. 1.4e+06; 1; Mismatches 0; Indel8
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/note= "This bond cyclises the peptide"
                                  Example 25; Page 47; 102pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU04541 standard; peptide; 8 AA.
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2000US-0204590P.
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Best Local Similarity 8/...
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diabetic retinopathy
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Cendron A;

Stacker S,

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(LUDW-) LUDWIG INST CANCER RES
    Hughes RA,
                                                                                                                                                 Disulfide-bond
                                                                                     Sequence 8 AA;
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9
                                                                                                                        26-SEP-2001
    Achen MG,
                                                                                                                                           Synthetic
                  residues.
                                                                                         Query Match
                                                                                                                    AAU04538;
                                                                                            Best Loc
Matches
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Whose 3 dimensional structure is modelled on the expose loop of human CVSCPD (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring betabet a carbon separation distances on opposite antiparallel strands of a peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides, dimeric bicyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with angiogenesis, a condition to Tymphangiogenesis in a mammal with a condition convacularisation or lymphangiogenesis, neovascularisation is diabetic retinopathy, psoriasis, arthropathy, hemangioma, vascularised malignant or benign tunnour, post-recovery creaborascular accident, post-rangioplasty restenosis, head, heat or cold trauma, substance-induced neovascular sequelae, hypertension induced neovascular sequelae, or chronic liver infection. The peptides are also used to modulate vascular permeability in a mammal (the mammal has a condition characterised by fluid a committed angiogenic disperse in mammal (the mammal has a condition characterised by fluid a committed more related angiogenic disperse in mammal (the mammal has a condition characterised by fluid a committed for modulate vascular permeability or brain the rephylement lines or in lungs, peritonal capitic, or brain the relation are determined to manual has a condition characterised by fluid accumulation in peripheral lines are also used to modulate accumulation; when peritons are need to modulate accumulation in a mammal has a condition characterised by fluid accumulation in the peripheral lines are also used to modulate accumulation; when peritons are need to modulate accumulation in the peripheral lines are also used to modulate accumulation in the peripheral lines are also used to modulate accumulation in the peripheral lines are also used to modulate accumulation in a mammal has a condition of the liver. Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine treat a sequence represents a monomeric monocyclic peptide of the invention, or brain. The peptides are used to image blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are used to interfere with at least one biological activity induced by VGGF, VGGF-C or -D and are also used in combination with an anti-inflammatory agent, to treat a chronic inflammation, especially rheumatoid arthritis, psoriasis and diabetic retinopathy Example 25; Page 47; 102pp; English WPI; 2001-442248/47.

ö Gaps ; 0 Score 42; DB 4; Length 8; Pred. No. 1.4e+06; 2; Mismatches 0; Indels 91.3%; 75.0%; Conservative 1 CNEESLIC 8 Local Similarity

|||||::| 1 CNEESVVC

AAU04538 standard; peptide; 8 AA.

· 0

Gaps

. 0

to treat a

VEGF based monocyclic peptide 16. (first entry)

Human; VEGF; vascular endothelial growth factor; angiogenesis; neovascularisation; lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic.

1. .8 /note= "This bond cyclises the peptide" Location/Qualifiers

Human; VEGF; vascular endothelial growth factor; angiogenesis; neovascularisation; lymphangiogenesis; psoriasis; tumour;

VEGF based monocyclic peptide 18.

(first entry)

26-SEP-2001

MAXEX EX AX AX

AAU04540;

AAU04540 standard; peptide; 8 AA

The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human VESPD (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring betace carbon separation distances on opposite antiparallel strands of a peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior neovascularisation or lymphangiogenesis in a mammal with a condition characterised by angiogenesis, neovascularisation or lymphangiogenesis, neovascularisation or lymphangiogenesis, arthropathy, homangiome, head continued maintended prince the manner of the condition is diabetic retinopathy, psoriasis, arthropathy, homangiomens. Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine cerebrovascular accident, post-angioplasty restenosis, head, heat or col trauma, substance-induced neovascularisation of the liver, excessive hormone-related angiogenic dysfunction, diabetes induced neovascular sequelae, hypertension induced neovascular sequelae, or chronic liver infection. The peptides are also used to modulate vascular permeability in a mammal (the mammal has a condition characterised by fluid accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain. The peptides are used to image blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are used to interfere with at least one biological activity induced by VEGF, VEGF-C or -D and are also used in combination with an anti-inflammatory agent, to tree chronic inflammation, especially rheumatoid arthritis, psoriasis and 89.1%; Score 41; DB 4; Length 8; 75.0%; Pred. No. 1.4e+06; tive 2; Mismatches 0; Indels Cendron A; Example 25; Page 47; 102pp; English. Stacker S, (LUDW-) LUDWIG INST CANCER RES 18-JAN-2000; 2000US-0176293P. 16-MAY-2000; 2000US-0204590P. 18-JAN-2001; 2001WO-US001533. Conservative Hughes RA, diabetic retinopathy WPI; 2001-442248/47. 1 CNEESLIC 8 Local Similarity nes 6; Conserv CNDESTIC WO200152875-A1 Sequence 8 AA; 26-JUL-2001 Achen MG, residues. Query Match Matches AAU04540 RESULT g à

or cold

Synthetic

Achen MG,

residues.

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The peptide is conformationally constrained by groups attached to each side. The peptide mimics a beta turn and can bind to at least one HIV envelope protein, thus inhibiting infection. It inhibits the interaction between HIV envelope glycoproteins and human cell-surface protein CD4 by mimicking structures of CD4. See also AAR24950-R24959 and AAR25122. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                              "beta-turn or beta-turn mimic tetrapeptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conformationally constrained peptides used for inhibiting HIV - be mimicking the stereochemical regions of the CD4 receptor protein.
                                                                                                                                                              Human immunodeficiency virus; AIDS; envelope glycoproteins; CD4; cell surface protein; infection.
                                                                                                                                                                                                                                                                                                                                       "conformationally constraining gp."
                                                                                                                                                                                                                                                                                                                                                                                                                      "conformationally constraining gp.
                                                                                                                        Conformationally constrained HIV inhibitory peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RLD, Dixon JS,
Ryu SE, Truneh
                                                                                                                                                                                                                                                                         Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SMIK ) SMITHKLINE BEECHAM CORP. (UYCO ) UNIV COLUMBIA NEW YORK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example; Page 24; 37pp; English.
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50.0%;
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Kwong P, Peishoff CE, Ryu
                                                               (revised)
(first entry)
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/note=
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                                                                                                                                                                                                                                                                           Key
Disulfide-bond
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                                                             25-MAR-2003
04-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-JUN-1992.
                                                                                                                                                                                                                                  Synthetic
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                     AAR24954;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                          Peptide
                                                                                                                                                                                                                                                                                                                     Region
                                                                                                                                                                                                                                                                                                                                                                                                    Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kwong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY54526
  g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human vaces 3-dimensional structure is modelled on the expose loop of human conversed to the invention relates to a method of producing a monomeric monocyclic peptide by a measuring beta-conversed loop fragment from an exposed loop of a growth factor protein and cyclising the peptide with at least one amino acid deleted prior peptides, dimeric bicyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with angiogenesis.

The condition is diabetic relinopathy, psoriasis, arthropathy, chemangioma, vascularised malignant or benign tumour, post-recovery cerebrovascular accident, post-angioplasty restenosis, head, heat or cold trauma, substance-induced neovascular sequelae, or chronic liver sequelae, hypertension induced neovascular sequelae, or chronic liver communication. The peptides are also used to modulate vascular permeability in a mammal (the mammal has a condition characterised by luid accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain. The peptides are also used to indepte and lustic contracterised by luid accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain. The peptides are also used to indepte are used to interfere with at least one biological activity induced by VEGF. VEGF-C or -D and are also used in combination with an uni-inflammatory agent, to treat a decident of the liver and and activity induced by VEGF. Cor -D and are also used in combination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chronic inflammation, especially rheumatoid arthritis, psoriasis and
diabetic retinopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
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diabetes induced neovascular sequelae, rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 8;
                                                                                                                                              /note= "This bond cyclises the peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 39; DB 4; I
Pred. No. 1.4e+06;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                            Cendron A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 25; Page 47; 102pp; English
                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                            Stacker S,
                                                                                                                                                                                                                                                                                                                                                                                  (LUDW-) LUDWIG INST CANCER RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84.8%;
                                                                                                                                                                                                                                                                                                                     18-JAN-2000; 2000US-0176293P.
16-MAY-2000; 2000US-0204590P.
                                                                                                                                                                                                                                                                           18-JAN-2001; 2001WO-US001533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          Hughes RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-442248/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CNEESLIC 8
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Best Local Similarity
Matches 6; Conserv
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CNEDSFIC
                                                                                                                             Disulfide-bond
                                                                                                                                                                                          WO200152875-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8 AA;
                                                                                                                                                                                                                                    26-JUL-2001
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Kopple KD;

Hendrickson WA, A, Sweet RW;

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0
                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, CD4 protein, antigenic peptide, CDR2-like domain, apoptosis, syncytia formation, human immune deficiency virus, HIV binding;
                                             ;
0
                                             2; Indels
Length 8;
                                                                                                                                                                                                                                                                                                                                                                                      Human CD4 protein target antigenic peptide p1615.
Score 30; DB 2; I Pred. No. 1.4e+06;
                                             2; Mismatches
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AAR24954 standard; protein; 8 AA.

RESULT 6 AAR24954 ID AAR2

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thyroid stimulating hormone receptor; TSH; human; Homo sapiens; antibody;
                               thyroid stimulating hormone receptor; TSH; human; Homo sapiens; antibody; affinity; detection.
                                                                                                                                                                                                                                                                                                                                                                                                     Novel polypeptide(s) having affinity for the human TSH receptor antibody - used in detection of the TSH antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel polypeptide(s) having affinity for the human TSH receptor antibody - used in detection of the TSH antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptides with affinity to human TSH (thyroid stimulating hormone) receptor antibody are used for detection of the antibody. (See also AAR73201-592)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptides with affinity to human TSH (thyroid stimulating hormone) receptor antibody are used for detection of the antibody. (See also AAR73201-592)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 26; DB 2;
Pred. No. 1.4e+06;
1; Mismatches 1
                                                                                                                                                                                                                                                                                                               MITP ) MITSUBISHI PETROCHEMICAL CO LID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MITP ) MITSUBISHI PETROCHEMICAL CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human TSH receptor (residues 291-298).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 25; 54pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Page 25; 54pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR73350 standard; peptide; 8 AA.
                                                                                                                                                                                                                                93JP-00240853
                                                                                                                                                                                                                                                                        93JP-00240853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              h 56.5%;
Similarity 66.7%;
4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93JP-00240853
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                                                                                                                                                                                                                                                                                                                                                            WPI; 1995-167251/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      affinity; detection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1995-167251/22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 4; Conserv
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CNESSM 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 8 AA;
                                                                                                                                       JP07089991-A
                                                                                                                                                                                                                             28-SEP-1993;
                                                                                                                                                                                                                                                                      28-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JP07089991-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-SEP-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-DEC-1995
                                                                                                                                                                                  04-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-APR-1995.
                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR73350;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents a target antigenic peptide derived from the CDR2-like domain of the human CD4 protein. The peptide is cyclised by the CDR2-like domain of cysteine residues at either end. The specification describes antigenic peptides derived from the CDR2-like domain of CD4 ending a coids 27-66 of ANY54500). These antigenic peptides present neutralising receptor/co-receptor effects sites of the CDR2-like domain. The peptides evoke effective antibody responses by having optimised sitespecificity. The induced antibodies block human immune deficiency virus (HVV) binding and syncytia formation. They may also block CD4-class II interactions with other cells deliver signals to T cells (inhibiting normal CD4+-mediated immunoregulatory functions) or induce apportises of containing the antiggament of T cell receptors. Conjugates and peptides containing the antiggament of T cell receptors. Conjugates and peptides containing the antiggament of T cell receptors. Conjugates and peptides containing the antiggament of T cell surface complexes, peptides containing the antiggament of T cell surface complexes, conformation to generate antibodies against CD4 and thus HIV infection, but a specially to prevent binding of HIV to CD4 and thus HIV infection, con autoimmune diseases (rheumatoid arthritis, systemic lupus corrections which are broadly neutralising against primary isolates from all classes of HIV-1 and of HIV-2. The peptides may include a promiscuous corrections are peptides may include a promiscuous corrections and includes which are broadly neutralising against primary isolates from all classes of HIV-2 and genetically diverse subjects
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö

    .8 /note= "this peptide is conformationally restricted by
cyclisation"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New antigenic peptide from the CDR2 domain of CD4, for immunization against e.g. human immune deficiency virus.
CD4-Class II interaction; immunisation; CD4 surface complex; immune response; transplant rejection; autoimmune disease; cyclic; rheumatoid arthritis; systemic lupus erythematosus; psoriasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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Pred. No. 1.4e+06;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human TSH receptor (residues 301-308).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure, Page 63; 106pp; English.
                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR73351 standard; peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                         (UNBI-) UNITED BIOMEDICAL INC
                                                                                                                                                                                                                                                                                                                                                     99WO-US014030.
                                                                                                                                                                                                                                                                                                                                                                                              98US-00100409.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65.2%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-DEC-1995 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-160579/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CNOGSFLC
                                                                                                                                                                         Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 8 AA;
                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                   21-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                              20-JUN-1998;
                                                                                                                                                                                                                                                             W09967294-A1
                                                                                                                                                                                                                                                                                                          29-DEC-1999
                                                                                        Synthetic
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Matches

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RESULT 8
AAR73351
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AC AAR
XX
DT 12-1
XX
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Wang

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Gaps

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Matches

XX OS

RESULT 10

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The present invention relates to polypeptides that bind cellular receptors for vascular endothelial growth factors (VEGFs), the polymucleotides encoding them, and their use for identifying agents that modulate interactions between VEGFs and their receptors. VEGFs and their receptors play an important role in vasculogenesis, the development of the embryonic vasculature from early differentiating endothelial cells and angiogenesis, the process of forming new blood vessels from presents include cancers, abnormal angiogenesis, receptors may be used to treat dysfunction of the endothelial cell regulatory proliferative retinopathies, age-related macular degeneration, rheumatoid arthritis and psoriasis. The polypeptides of the invention exhibit unique arthritis and psoriasis. The polypeptides of the invention exhibit unique arthritis represent the peptides Alvos which are encoded by human VEGFA forward primers used in the methods of the present invention
                                                                                                                Human, vascular endothelial growth factor, VEGP-A; vasculogenesis, angiogenesis, blood vessel, cancer, proliferative retinopathy; psoriasis, age-related macular degeneration; rheumatoid arthritis; cardiovascular;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Polypeptides that bind cellular receptors for vascular endothelial growth factors, polynucleotides encoding them.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 26; DB 4; Length 8;
Pred. No. 1.40+06;
1; Mismatches 1; Indels
                                                                                     Peptide A6 encoded by human VEGF-A forward primer A6-F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR80365 standard; peptide; 8 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 9; Fig 7C; 261pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                               (LUDW-) LUDWIG INST CANCER RES. (LICN) LICENTIA OY.
                                                                                                                                                                                                                                                                                                                                                                            25-FEB-2000; 2000US-0185205P.
18-MAY-2000; 2000US-0205331P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56.5%;
                                                                                                                                                                                                                                                                                                                                          26-FEB-2001; 2001WO-US006113
                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alitalo K, Jeltsch MM;
                                                                                                                                                                              primer; mutant; mutein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-536640/59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAS12807
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                                                                                                                                                                                                                                                                  WO200162942-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 8 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-APR-1996
                                                                                                                                                                                                                Homo sapiens
                                                 21-NOV-2001
                                                                                                                                                                                                                                                                                                        30-AUG-2001
                                                                                                                                                                                                                                   Synthetic
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             AAU08451;
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δ
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                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence is an immunogenic fragment of feline immunodeficiency virus (FIV) glycoprotein 130. Peptides AAY57038-Y57039 (also fragments of gp130) are used in the invention as capture polypeptides when diagnosing FIV infection. The invention relates to an antibody binding composition immunogenic fragment of FIV gag precursor p55, and a second fragment which is part of the env precursor p55, and an antibody-binding which is part of the env precursor gp130, and an antibody-binding performing an assay which determines whether a feline is infected with Immunodeficiency Virus infection
                                                                                                                                                                                                                                                                                                                                                                                           Feline immunodeficiency virus; FIV; infection; diagnosis; gpl30; p55; immunogenic fragment; antibody; env precursor; gag precursor; cat; antibody binding composition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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                                                                                     1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 26; DB 3; Length 8;
Pred. No. 1.4e+06;
                                                 Length 8;
                                                                                                                                                                                                                                                                                                                                                               Feline immunodeficiency virus immunogenic fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Diagnosing Feline Immunodeficiency Virus infection.
                                                                      Pred. No. 1.4e+06;
                                                   Score 26; DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                       1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               O'connor TP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure, Page 4, 15pp; English
                                                                                                                                                                                                                                                    AAY57040 standard, peptide, 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Feline immunodeficiency virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99EP-00303760,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98US-0085615P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98US-00089878
                                                   56.5%;
                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                         4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (IDEX-) IDEXX LAB INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mermer B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CNEESLIC 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-025671/03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CNONOFFC
                                                                                                                           1 CNEESL 6
                                                                                                                                                CNESSM
                 Sequence 8 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 8 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-JUN-1998;
                                                                                                                                                                                                                                                                                                                           21-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EP962774-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Groat RG,
                                                                                                                                                                                                                                                                                        AAY57040;
                                                     Query Match
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Gaps

; 0

Protein polymeric adhesion substrate glutamine donor peptide #15.

AAU08451 standard; peptide; 8 AA.

RESULT 11 AAU08451 ID AAU08

Matches

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95WO-US002728 94US-00205518

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Protein polymers comprising repeating units and sequences - capable of enzyme-catalysed covalent bond formation useful as a biocompatible material for wound closure and tissue repair.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein polymer; adhesive sealant; wound healing; cross-linking.
                                                                                                                       (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
                              protein polymer adhesive substrate
                                                                                                                                                                                                   Example 9; Page 75; 138pp; English
                                                                                                                                                                                                                                                                                                                                                                                            AAW49750 standard; peptide; 8
                                                                                                                                                                                                                                                                                                                            3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glutamine donor peptide
                                                                                                                                                     WPI; 1995-320413/41
                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                                                                                                                                          1 CNEESLIC
                                                                                                                                                                                                                                                                                                                                                        1 ČGQSKVÍČ
                                                                                                                                                                                                                                                                                            Sequence 8 AA;
                                                                                                        03-MAR-1994;
                                                            WO9523611-A1
                                                                                         03-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-MAR-1995;
                                                                          08-SEP-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                            25-MAR-2003
12-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JS5773577-A
                                                                                                                                       Cappello J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-JUN-1998
                                             Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                             AAW49750;
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This is an example of a glutamine donor peptide that can be utilised in novel recombinant protein polymers of the invention. Such polymers (see AAW49710-28) typically comprise a repetitive amino acid backbone of repetitive units having a collagen, fibroin, elastin or keratin motif at least 2 enzyme recognition sequences comprising a glutamine and/or lysine capable of enzyme catalysed isopeptide formation. The polymers are capable of covalent crosslinking by enzymatic reaction to form products which set quickly and have good adhesive properties and high strength. They can be used as medical adhesives and sealants, in the closure of wounds and repair of damaged tissues, prosthesis coatings, drug depots, and matrices for the transplantation of cells. (Updated on 25-MAR-2003 to
                                                                                          New recombinant protein polymers - containing naturally occurring repetitive units for crosslinking by enzymes, useful as medical adhesives
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New peptides which selectively home to organs or tissues, used for, e.g. identifying target ligands and for therapy of pathological conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homing peptide; organ; tissue; lung; pancreas; skin; retina; MDP; prostate; ovary; lymph node; adrenal gland; liver; gut; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Membrane dipeptidase-binding lung homing peptide #15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 25; DB 2; I Pred. No. 1.4e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ruoslahti EI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 6; Page 144; 193pp; English
                                                                                                                                and sealants, depots and matrices
                                                                                                                                                                 Example 9; Col 49; 70pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY48644 standard; peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-00042107.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-US005284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-00258754
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rajotte D, Pasqualini
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                membrane dipeptidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BURN-) BURNHAM INST
                                                     WPI; 1998-387091/33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-571717/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                      correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CNEESLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CGQSKVIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 8 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9946284-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-SEP-1999.
                   Cappello J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY48644;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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à
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The peptides AAR80351-70 are examples of glutamine donor peptides which can be used to generate protein polymeric adhesion substrate (PPAS) contg. repeats of non-fibrin cross-linking donor peptide sequences (see AAR80345-50 for examples of PRAS proteins). The PPAS proteins can be used as substrates in enzymatic cross-linking reactions catalysed by a transglutaminase enzyme e.g. Factor VIII or XIII. The polymers can be used in biological systems where in situ formation of a biocompatible material with structural integrity is required e.g. as medical adhesives and sealants or for wound closure or tissue repair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
         Pendent group; repeating unit; enzyme recognition site; sealant; fibrin; enzymatic cross-linking; biocompatible material; structural integrity; medical adhesive; wound closure; tissue repair; transglutaminase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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, DB 2; Leus.

Score 25; DB 2 Pred. No. 1.4e+ 2; Mismatches

54.3%;

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(revised)
(first entry)

95US-00397633 94US-00205518

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The present invention describes peptides that selectively home to a tissue or organ. The peptides can be used for identifying an organ or tissue, for identifying a target molecule expressed by an organ or tissue or for treating an organ or tissue pathology, where the organ or tissue is selected from prostate, lung, skin, retina, pancreas, gut, ovary, adrenal gland, liver, and lymph node. The peptide bind to the membrane dipeptidase (MDP). AAY48618 to AAY49066 represent sequences which are used in the exemplification of the present invention. (Updated on 20-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                  Targeting peptide; cancer; Hodgkin's disease; cytostatic; immunosuppressive; anti-inflammatory; antiarthritc; antiviral; antiatheroscalerotic; antidatebetto; antibacterial; diabetes mellitus; inflammatory disease; arthritis; atherosclerosis; cancer; autoimmune disease; bacterial infection; viral infection.
                                                                                                                                                            Score 25; DB 2; Length 8;
Pred. No. 1.4e+06;
1; Mismatches 3; Indels
                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                             ABG35021 standard; peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                             Endostatin targeting peptide #20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-SEP-2000; 2000US-0231266P. 17-JAN-2001; 2001US-00765101.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-SEP-2001; 2001WO-US027702
                                                                                                                                                               54.3%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                    15-JUL-2002 (first entry)
                                                                                                                                                                                           4; Conservative
                                                                                                                                                                                                                    1 CNEESLIC 8
                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                            1 CGNETLRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200220722-A2
                                                                                                                                       Sequence 8 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-MAR-2002.
                                                                                                                                                                                                                                                                                                                                         ABG35021;
                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                   RESULT 15
                                                                                                                                                                                                                                                                                                                           g
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This invention relates to a novel method for identifying disease targeting peptides. The method comprises exposing a sample from an organ, tissue or call type of interest, to a phage display library and recovering phage bound to the sample (the phage expresses targeting peptides). The peptides identified by the method of the invention may have cytostatic, immunosupressive, anti-inflammatory, antiarthritic, antiatherosclerotic, antidabetic, antibacterial and antiviral activities. The methods and composition are useful for identifying targeting peptides and one or more receptors for a targeting peptide. The targeting peptides are used for selective delivery of therapeutic agents, including gene therapy vectors and fusion proteins, to specific organs, tissues, or cell types in subject. The targeting peptide may also be used

Identifying targeting peptides useful for treating e.g. diabetes mellitus, inflammatory diseases, cancer, or autoimmune diseases, comprises exposing a sample to a phage display library and recovering phage bound to the sample.

(TEXA) UNIV TEXAS SYSTEM.

Arap W, Pasqualini R; WPI; 2002-383050/41. Claim 56; Page 242; 298pp; English.

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for treating diseases such as diabetes mellitus, inflammatory diseases, arthritis, atherosclerosis, cancer, autoimmune diseases, bacterial and viral infections and Hodgkin's disease. The present sequence represents targeting peptide of the invention
                                                                                                                                                             Gaps
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                                                                                                                                                          3; Indels
                                                                                                                        Score 25; DB 5; Length 8;
Pred. No. 1.4e+06;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                               5, 2004, 10:38:28
                                                                                                                            Query Match
Best Local Similarity 37.5%;
Matches 3; Conservative
                                                                                                                                                                                                                                                                               Search completed: September
                                                                                                                                                                                                1 CNEESLIC 8
                                                                                                                                                                                                                                CSRSSFLC
                                                                                              Sequence 8 AA;
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Gaps

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Sequence

Sequence 3664, Ap Sequence 3664, Ap Sequence 3665, Ap Sequence 92, Appl Sequence 1071, Ap Sequence 1071, Ap Sequence 3624, Ap Sequence 3624, Ap Sequence 363, Ap Sequence 363, Ap Sequence 2242, Ap Sequence 2246, Ap

Sequence 77, Appl Sequence 36, Appl Sequence 175, App Sequence 9, Appli Sequence 39, Appli Sequence 29, Appli

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Gaps

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APPLICANT: ACHEN, Marc
APPLICANT: ACHEN, Marc
APPLICANT: STACKER, Steven
APPLICANT: STACKER, Steven
APPLICANT: TIGGRES, Richard
APPLICANT: CENDRON, Angela
TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
FILE REFERENCE: 1064/48505 Achen et al
CURRENT APPLICATION NUMBER: US/09/761,636A
CURRENT FILING DATE: 2000-01-18
PRIOR APPLICATION NUMBER: US 60/176,293
PRIOR PLING DATE: 2000-01-18
PRIOR PLING DATE: 2000-05-16
PRIOR PLING DATE: 2000-05-16
SPIOR FILING DATE: 2000-05-16
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 46; DB 9; Length 8; larity 100.0%; Pred. No. 1.2e+06; Conservative 0; Mismatches 0; Indels
US-10-651-723-457

US-10-645-761-457

US-10-665-696-457

US-10-653-048-457

US-10-053-048-457

US-10-006-869-3664

US-10-006-869-3665

US-10-006-869-3665

US-10-006-869-1071

US-10-006-869-1071

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US-10-006-869-1071

US-10-006-869-1085

US-10-006-869-1085

US-10-006-869-2242

US-10-006-869-2245

US-10-006-869-2246

US-10-006-869-2346

US-10-006-869-2160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 20, Application US/09761636A Patent No. US20020065218A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6, Application US/09761636A Patent No. US20020065218A1 GENERAL INFORMATION:
      LENGTH: 8
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CNEESLIC 8
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Best Local Similarity
Matches 8; Conserv
    US-09-761-636A-20
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US-09-761-636A-6
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Sequence 20, Appl
Sequence 12, Appl
Sequence 13, Appl
Sequence 13, Appl
Sequence 142, Appl
Sequence 14, Appl
Sequence 25, Appl
Sequence 25, Appl
Sequence 27, Appl
Sequence 27, Appl
Sequence 82, Appl
                                                                                                                            September 5, 2004, 10:38:54; Search time 67 Seconds (without alignments) 37.620 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Published Applications AA:*

| cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO6_NEW PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO6_NEW PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO7_NEW PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
            GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-761-636A-6
US-09-761-636A-20
US-09-761-636A-12
US-09-761-636A-13
US-09-765-006A-133
US-09-795-006A-142
US-09-795-006A-142
US-09-795-006A-142
US-09-795-006A-145
US-09-185-908-115
US-09-185-908-115
US-10-609-217-457
US-10-609-217-457
US-10-609-217-457
US-10-609-217-457
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US-10-609-217-457
US-10-609-217-457
US-10-609-217-457
US-10-609-217-457
                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                         1298764 seqs, 315065143 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                      OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                            BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                US-09-761-636A-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query
Match Length
                                                                                                                                                                                                                                                    1 CNEESLIC 8
                                                                                                                                                                                                                                                                                                                                                                                                                                     Minimum DB seq length: 0 Maximum DB seq length: 8
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Perfect score:
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Gaps

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Sequence 133, Application US/09795006A
Patent No. US20020151680A1
GENERAL INFORMATION
GENERAL INFORMATION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR
TITLE OF INVENTION: RNOTHELIAL GROWTH FACTOR DNAS AND PROTEINS
TITLE OF INVENTION: RNOTHELIAL GROWTH FACTOR DNAS AND PROTEINS
TITLE OF INVENTION: BNOTHELIAL GROWTH FACTOR DNAS AND PROTEINS
CURRENT APPLICATION NUMBER: US/09/795,006A
CURRENT FILING DATE: 2001-02-26
PRIOR APPLICATION UNDER: US 60/205,331
PRIOR PILING DATE: 2000-05-18
PRIOR APPLICATION NUMBER: US 60/185,205
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; Sequence 21, Application US/09761636A
; Patent No. US20020065218A1
; GRENERAL INFORMATION:
    APPLICANT: ACHEN, Marc
    APPLICANT: STRAKERS, Steven
; APPLICANT: CENDRON, Angela
    TITLE OF INVENTION: VEGF-D/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
    TUCKRENT APPLICANTON NUMBER: US/09/761,636A
    CURRENT PILING DATE: 2001-01-18
; FRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; WUMBER OF SEQ ID NOS: 34
; SEQ ID NOS: 34
; SEQ ID NO 2.
TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR FILE REFERENCE: 1064/48505 Achen et al CURRENT APPLICATION NUMBER: US/09/761,636A CURRENT FILING DATE: 2001-01-18 PRIOR PLING DATE: 2001-01-18 PRIOR PLING DATE: 2000-01-18 PRIOR PLING DATE: 2000-01-18 PRIOR PLING DATE: 2000-05-16 SOWINGER: US 60/204,590 PRIOR PLING DATE: 2000-05-16 SOWINGER: PRIOR DAT
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75.0%; Pred. No. 1.2e+06;
:ive 1; Mismatches 1;
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Pred. No. 1.2e+06;
2; Mismatches 0;
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; ORGANISM: synthetic construct
US-09-761-636A-21
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Best Local Similarity 75.0
Matches 6, Conservative
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Best Local Similarity 75.0
Matches 6; Conservative
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; Sequence 22, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION
; APPLICANT: ACHEN, Marc
; APPLICANT: HUGHER, Richard
; APPLICANT: HUGHER, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US 60/176,536A
; CURRENT FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; RROR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SEQ ID NOS: 34
; SEQ ID NO 22
                                                          APPLICANT: ACHEN, Marc
APPLICANT: ACHEN, Marc
APPLICANT: STACKEN, Steven
APPLICANT: CENDRON, Angela
TITLE OF INVENTION: VEGF-D/VEGF PEPTIDOMIMETIC INHIBITOR
FILE REFERENCE: 1064/48505 Achen et al.
CURRENT APPLICATION NUMBER: US/09/761,636A
CURRENT FILING DATE: 2001-01-18
PRIOR APPLICATION NUMBER: US 60/176,293
PRIOR FILING DATE: 2000-01-18
PRIOR FILING DATE: 2000-01-18
PRIOR FILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin version 3.0
SOFTWARE: Patentin version 3.0
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US-09-761-636A-22
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Best Local Similarity 87.5%;
Matches 7; Conservative
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APPLICANT: STACKER, Steven
APPLICANT: HUGHES, Richard
APPLICANT: CENDRON, Angela
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Best Local Similarity 75...
Best Local 6; Conservative
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                                    GENERAL INFORMATION:
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| Sequence 142, Application US/09795006A |
| Patent No. US20020151680A1 |
| GENERAL INFORMATION: ATTENDED AND METHODS INVOLVING HYBRID VASCULAR |
| TITLE OF INVENTION: MTPERIALS AND METHODS INVOLVING HYBRID VASCULAR |
| TITLE OF INVENTION: MTPERIALS AND METHODS INVOLVING HYBRID VASCULAR |
| TITLE OF INVENTION: ENDOTHELIAL GROWTH FACTOR DNAS AND PROTEINS |
| TITLE OF INVENTION: ENDOTHELIAL GROWTH FACTOR DNAS AND PROTEINS |
| TITLE OF INVENTION: ENDOTHELIAL GROWTH FACTOR DNAS AND PROTEINS |
| TITLE OF INVENTION: ENDOTHELIAL GROWTH FACTOR DNAS AND PROTEINS |
| FILE REFERENCE: 28967/359778 |
| PRIOR APPLICATION NUMBER: US 60/205,331 |
| PRIOR APPLICATION NUMBER: US 60/205,331 |
| PRIOR APPLICATION NUMBER: US 60/185,205 |
| NUMBER OF SEQ ID NOS: 175 |
| NUMBER OF SEQ ID NOS: 175 |
| NUMBER PATENT NOS: 175
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US-10-363-208-108
US-10-363-208-108
Sequence 108 Application US/10363208
Publication No. US20040048243A1
GENERAL INFORMATION:
APPLICANT: Board of Regents, The University of Texas System
TITLE OF INVENTION:
PILE REFERENCE: 055774. P005PCT
CURRENT APPLICATION NUMBER: US/10/363,208
CURRENT PILING DATE: 2003-03-07
NUMBER OF SEQ ID NOS: 273
SOFTWARE: Patentin version 3.1
SEQ ID NO 108
                                                                                                                                                                                                                                                                            OTHER INFORMATION: Description of Artificial Sequence: synthetic OTHER INFORMATION: peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 8;
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Pred. No. 1.2e+06;
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CTHER INFORMATION: synthetic construct US-10-363-208-108
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
FEATURE:
PRIOR FILING DATE: 2000-02-25
NUMBER OF SEQ ID NOS: 175
SOFTWARE: PATENTIN VEY: 2.0
SEQ ID NO 133
LENGTH: 8
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ORGANISM: Artificial Sequence
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1 CSRSSFLC 8
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Best Local Similarity
Matches 4; Conserv
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CNDEGL 8
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LENGIH: 8
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: CHERMANN, JEAN-CLAUDE
APPLICANT: CHERMANN, JEAN-CLAUDE
APPLICANT: CHERMANN, JEAN-CLAUDE
APPLICANT: GALEA, PASCALE
APPLICANT: GALEA, PASCALE
TITLE OF INVENTION: VACCINE ACAINST INFECTIOUS AGENTS HAVING AN
TITLE OF INVENTION: DIAGNOSIS
CURRENT PALLICATION NUMBER: US/09/827,345
CURRENT FILING DATE: 1096-06-23
PRIOR PELLING DATE: 1996-06-28
PRIOR PELLING DATE: 1996-02-19
PRIOR FILING DATE: 1996-02-19
PRIOR PELLING DATE: 1996-03-19
PRIOR PELLING DATE: 1996-04-30
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OTHER INFORMATION: Description of Artificial Sequence: synthetic OTHER INFORMATION: peptide
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Fatent No. US20020168363A1
GENERAL INFORMATION:
APPLICANT: FEIGE, ULRICH
APPLICANT: KOHNO, TADAHIKO
APPLICANT: LACEY, DAVID LEE
APPLICANT: LACEY, DAVID LEE
TILE REFERENCE: A-689A
CURRENT APPLICATION NUMBER: US/09/840,277
CURRENT FILING DATE: 2001-08-14
PRIOR RELICATION NUMBER: 60/198,919
PRIOR FILING DATE: 2000-04-21
PRIOR APPLICATION NUMBER: 60/198,919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-827-345-14
; Sequence 14, Application US/09827345
; Publication No. US20030021800A1
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                                                                                                                                                           Query Match
Best Local Similarity 66.7
Matches 4; Conservative
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Best Local Similarity
Matches 4; Conserv
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Best Local Similarity 25.0
Matches 2; Conservative
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1 CRASAMVC 8
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                                                                                                                                                                                                                                                                      1 CWDDGLMC 8
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US-10-363-208-74
SEQ ID NO 457
LENGTH: 8
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Publication No. US20020193294A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Blaschuk,
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CLAUDIN-MEDIATED
TITLE OF INVENTION: CMOUNTIONS
FILE REFERENCE: 100086.409
CURRENT FILING DATE: 1998-11-03
NUMBER OF SEQ ID NOS: 269
SEQ ID NOS: 269
SEQ ID NO 115
LENGTH: 8
LENGTH: 8
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OTHER INFORMATION: synthesis based on mouse claudin-2 sequence
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Publication No. US20040044188A1
GENERAL INFORMATION:
APPLICANT: EIGH, CHUNN-FA
APPLICANT: CHEETHAM, JANET C.
APPLICANT: GENERAL C.
APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
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                                                                                                                                                                                                                                50.0%; Score 23; DB 9; Length 8; 37.5%; Pred. No. 1.2e+06; ive 3; Mismatches 2; Indels
                                                                                                                                                                        ), OTHER INFORMATION: Integrin antagonist peptide
US-09-840-277-25
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CURRENT APPLICATION NUMBER: US/06-27
CURRENT FILING DATE: 2003-06-27
PRIOR APPLICATION NUMBER: US/09/428,082B
PRIOR APPLICATION NUMBER: 60/105,371
PRIOR APPLICATION NUMBER: 60/105,371
PRIOR FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 1133
SOFTWARE: PATENTIN VERSION 3.1
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                                                                                                             TYPE: PRT ORGANISM: Artificial Sequence
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                         NUMBER OF SEQ ID NOS: 135
SOFTWARE: Patentin version 3.1
SEQ ID NO 25
LENGTH: 8
        PRIOR FILING DATE: 2000-05-03
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1 CWDDGLMC 8
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Best Local Similarity
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US-10-609-217-457
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US-09-185-908-115
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US-10-363-208-82
US-10-363-208-82
US-10-363-208-82
Sequence 82, Application US/10363208
Publication No. US20040048243A1
GENERAL INFORMATION:
APPLICANT: Board of Regents, The University of Texas System
TITE POR INVENTION: Methods and Compositions for In Vitro Targeting
FILE REFERENCE: 050774. POOSPCT
CURRENT APPLICATION NUMBER: US/10/363,208
CURRENT FILING DATE: 2003-03-07
NUMBER OF SEQ ID NOS: 273
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATE BOARD OF REGENTS, The University of Texas System TITLE OF INVENTION: Methods and Compositions for in Vitro Targeting FILLE REFERENCE: 005774-0005PCT CURRENT APPLICATION NUMBER: US/10/363,208 CURRENT APPLICATION NUMBER: US/10/363,208 NUMBER OF SEQ ID NOS: 273 SOFTWARE: Patentin version 3.1 SEQ ID NO 74
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                                                                                                                              Score 23; DB 12; Length 8; Pred. No. 1.2e+06; 3; Mismatches 2; Indels
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25.0%; Pred. No. 1.2e+06;
tive 3; Mismatches 3;
                                             FEATURE:
; CTHER INFORMATION: INTEGRIN-BINDING PEPTIDE US-10-609-217-457
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; LOCATION: (1)..(8)
; OTHER INFORMATION: synthetic construct
US-10-363-208-82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , LUCATION: (1)..(8)
; OTHER INFORMATION: synthetic construct US-10-363-208-74
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 74, Application US/10363208 Publication No. US20040048243A1 GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                        Query Match 50.0
Best Local Similarity 37.5
Matches 3; Conservative
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Matches 2; Conservative
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RESULT 15
US-10-632-388-457
Sequence 457, Application US/10632388
Publication No. US20040053845A1
GENERAL INPORMATION:
APPLICANT: FEIGE, ULRICH
APPLICANT: LIU, CHUAN-FE
APPLICANT: LIU, CHUAN-FE
APPLICANT: BOONE, THOMAS CHARLES
TILLE REFERENCE: A-57
CURRENT APPLICATION NUMBER: US/10/632,388
FILE REFERENCE: A-57
CURRENT PILING DATE: 2003-07-31
FRIOR PILING DATE: 1999-10-22
FRIOR FILING DATE: 1999-10-23
NUMBER OF SEQ ID NOS: 1133
SOFTWARE: PRECENTION NUMBER: 60/105,371
FRIOR FILING DATE: 1999-10-23
NUMBER OF SEQ ID NOS: 1133
SOFTWARE: PRECENTION NUMBER: 60/105,371
FRIOR FILING DATE: 1999-10-23
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1 CNEESLIC 8 | | :::| | 1 CRASAMVC 8
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Search completed: September 5, 2004, 10:44:41 Job time : 67 secs

1 CNEESLIC 8 | :: |:| 1 CWDDGLMC 8

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Sequence 27, Appl Sequence 10, Appl Sequence 49, Appl Sequence 49, Appl Sequence 14, Appl Sequence 13, Appl Sequence 13, Appl Sequence 214, Appl Sequence 214, Appl Sequence 214, Appl Sequence 214, Appl Sequence 12, Appl Sequence 14, Appl Sequence 165, Appl Sequence 1
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1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/pcarus_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                        389414 segs, 51625971 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                              OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Match Length
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1 CNEESLIC 8
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Perfect score:
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No.
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225 36, 38, 39, 39, 39, 39, 39, 39, 39, 39, 39, 39	AND	Gaps
Sequence Seq	INFECTION	.0
	OF HIV INF	Length 8; ; Indels
S-09-258-754-256 S-09-042-107-36 S-09-042-107-48 S-09-042-107-256 S-09-187-859-1071 S-09-187-859-1071 S-09-839-542B-1071 S-09-839-542B-1071 S-09-839-542B-362 S-09-722-250D-36 S-09-722-250D-36 S-09-722-250D-36 S-09-722-250D-36 S-09-722-250D-36 S-09-722-250D-36 S-09-722-250D-36 S-09-187-859-365 S-09-187-859-365 S-09-187-859-365 S-09-187-859-365 S-09-839-542B-965 S-09-839-542B-965	ALIGNMENTS 109A MPOSITION FOR 1 AND TREATMENT CORDERS 10, 409A 1-4154	ore 30; DB 3; ed. No. 3e+05; Mismatches 2
8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	tion US/09100409A chang Yi N: PEPTIDE COMPO N: IMMUNE DISORD SS: 64 SS: 64 SNESS: SAN & FINNEGAN KR Avenue TO COMPO TO CO	MATION: 8800 9: 27: 5: 27: 18: 8: 27: 8: 27: 8: 27: 8: 27:
α	T. 1 1-100-409A-27 PUBLICATION (6090388) BAPLICANT: WARDICATION US/0910044 BAPLICANT: WAND, CHANG XI TITLE OF INVENTION: PREVENTION TITLE OF INVENTION TITLE OF INVENTION: BARE COMPUTER: PREVENTION DATA: REGISTRATION NUMBER: US/09/100 REGISTRATION NUMBER: 1153 REGISTRATION NUMBER: 1153	TELECOMMUNICATION INFORMATION: TELEPHONE: 212-758-4800 TELEPHONE: 212-758-4800 INFORMATION FOR SEQ ID NO: 27: SEQUENCE CHARACTERISTICS: LENGTH: 8 amino acids TYPE: amino acid TYPE: amino acid TYPE: peptide 100-LOGY: linear MOLECULE TYPE: peptide 100-409A-27 Set Local Similarity 50.0%; pr stches 4; Conservative 2; ICHERSLIC 8
4444444444444444 77777777777777777	A-27 , Applicat 6090388 6090388 TT: Wang, TT: Wang, INVENTION INVENTION NUBNICE ADD SEE: MORE 345 Par New York	CUNICATION CONDE: 212-72 XX: 212-75 N FOR SEQ CHARACTER AND O O O O O O O O O O O O O O O O O O O
	RESULT 1 1 Sequence 27, Application 1 Patent No. 6090388 1 PATENTE No. 6090388 1 TILLE OF INVENTION: 1 TILLE OF INVENTION	TELECOMMUNICA TELEPHONE: TELEPHONE: TELEPAX: 2. INFORMATION FOR SEQUENCE CHARL LENGTH: 8 in TYPE: amin TYPE: amin TYPE: 09-100-409A-27 uery Match est Local Simila atches 4; Cc
7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	RESULT 1 US-09-100-4(Sequence) Patent No Patent No TITLE (TITLE	TELECOMY TELEPEN TELEPEN TELEPEN TELEPEN TOPORATIC SEQUENCE TYPE:

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1 CNEESLIC 8
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1 CGNETLRC 8
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1 CGQSKVIC 8
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US-08-397-633A-100
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US-09-042-107-49
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US-09-258-754-49
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                                              Query Match
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RESULT 2
US-09-878-3
i Sequence 3, Application US/09089878
i Sequence 3, Application US/09089878
j Patent No. 6458528
i GENERAL INFORMATION:
APPLICANT: Groat, Randall G.
APPLICANT: Groat, Thomas P.
APPLICANT: Groat, Thomas P.
TITLE OF INVENTION: USING ENV/GAG POLYBEPTIDE MARKERS
TITLE OF INVENTION: UNBING ENV/GAG POLYBEPTIDE MARKERS
TITLE OF INVENTION: UNBING ENV/GAG POLYBEPTIDE MARKERS
THER REPERING DATE: 1998-06-03
BARLIER APPLICATION UNMBER: US 60/085,615
BARLIER PILLNG DATE: 1998-05-15
NUMBER OF SEQ ID NOS: 3
SOFTWARE PREFECT OF Windows Version 3.0
SEQ ID NO 3
LENGTH: B
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Patent No. 5773577;
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: PRODUCTS COMPRISING SUBSTRATESCAPABLE;
TITLE OF INVENTION: OF ENZYMATIC CROSS-LINKING
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLERK, HOHBACK, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STAFET: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 56.5%; Score 26; DB 4; Length 8; Best Local Similarity 37.5%; Pred. No. 38+05; Matches 3; Conservative 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Rowland, Bertram I
REGISTRATION NUMBER: 20,015
REFERENCE/DOCKET NUMBER: 20,015
REFERENCE/DOCKET NUMBER: 4.58848-1/BIR PROP-011-1
TELEPHONE: (415) 781-1989
TELEPHONE: (415) 781-1989
TELERS: (415) 781-299
INFORMATION FOR SEQ ID NO: 100: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA

COMPUTER READABLE FORM:
MEDIUTY TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/33A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Feline immunodeficiency virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 amino acide
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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION: 530
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US-08-397-633A-100
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; Sequence 49, Application US/09258754
; Patent No. 6174687
; GENERAL INFORMATION:
   APPLICAMT: Rasolatt, Erkki
   APPLICAMT: Rasolati, Erkki
   APPLICAMT: Rasolati, Enaita
   APPLICAMT: Rasolati, Mathods of Identifying Lung Homing Molecules Using
   TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
   TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
   TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
   TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
   TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
   TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
   TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
   TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
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   TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
   TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
   TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
   TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
   TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
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                                                                                                                     Indels
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Length 8;
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Score 25; DB 1;
Pred. No. 3e+05;
2; Mismatches
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           54.3%;
37.5%;
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Best Local Similarity 50.0.
Lag 4; Conservative
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THE TREATMENT AND
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AN INTRACELLULAR PHASE, COMPOSITION FOR THE TREATMENT PREVENTION OF HIV INFECTIONS, ANTIBODIES AND METHOD OF
                                                                                  APPLICANT: Rucelalti, Erkki
APPLICANT: Ragualini, Renata
TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
TITLE OF INVENTION: Tissues
FILE REFERENCE: P-LJ 45.4
FILE REFERENCE: P-LJ 45.4
CURRENT APPLICATION NUMBER: US/09/722,250D
CURRENT FILING DATE: 1998-03-13
PRIOR PILING DATE: 1998-03-13
NUMBER OF SCO ID NOS: 437
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 49
LENGTH: 8
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SOFTWARE:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,551
FILING DATE: 30-DEC-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR96/01006
FILING DATE: 28-JUN-1996
PRIOR APPLICATION NUMBER: FR 9507914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54.3%; Score 25; DB 4; 50.0%; Pred. No. 3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Chermann, Jean-Claude
APPLICANT: Le Contel, Carole
APPLICANT: Le Contel, Carole
APPLICANT: Galea, Pascale
TITLE OF INVENTION: VACCINE AGAINST INFECTI
TITLE OF INVENTION: AN INTRACELLULAR PHASE,
TITLE OF INVENTION: DIAGNOSIS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Wasshington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
US-09-722-250D-49
i Sequence 49, Application US/09722250D
Patent No. 6610651
GENERAL INFORMATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 6113902
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                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
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ATTORNEY/AGENT INFORMATION:
NAME: Granados, Patricia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Conservative
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COMPUTER READABLE FORM:
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Matches 4; Conserv
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APPLICANT: Cherman
APPLICANT: Le Cont
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Gaps
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Patent No. 5817750
GENERAL INFORMATION:
APPLICANT: RUCALDARLI, Erkki
APPLICANT: Pasqualini, Renata
TITLE OF INVENTION: Structural Mimics of RGD-Binding Sites
CORRESPONDENCE: 28
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                          DB 3; Length 7; 3e+05;
                                                                                                                                                                                                                                                                                                                                1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LIBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/520,535
FILING DATE: 28-AUG-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                        Score 23; DB
Pred. No. 3e+0
0; Mismatches
                   REFERENCE/DOCKET NUMBER: 65691/130
TELECOMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 1794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
REGISTRATION NUMBER: 33,683
                                                                                                                                                                                                                                                                                          50.0%;
                                                                       TELEFIX: (202)672-5399
TELEX: 904136
INFORMATION FOR EGQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                              4; Conservative
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Best Local Similarity 37.5
Matches 3; Conservative
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                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
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Best Local Similarity
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1 CWDDGLMC
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US-08-520-535-3
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RESULT 9

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                                                                            Conservative
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Best Local Similarity
Matches 4; Conserv
                            Query Match
Best Local Similarity
Matches 4; Conserv
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1 CHEGYLTC
                                                                                                                  1 CNEESLIC
                                                                                                                                                    1 CRHESSSC
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US-09-258-754-214
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US-09-258-754-42
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US-09-258-754-33
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Fatent No. 6174687
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Rajotte, Daniel
TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
TITLE OF INVENTION: Methods Dipeptidase
FILE REPERENCE: P-LJ 3443
CURRENT APPLICATION NUMBER: US/09/258,754
CURRENT APPLICATION NUMBER: US/09/258,754
CURRENT FILING DATE: 1999-03-13
MUMBER OF SEQ ID NOS: 452
SOFTWARE: PATENTIN VOS: 452
SOFTWARE: PATENTIN VOS: 452
SEQ ID NO 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                            APPLICANT: Ruoslahti, Erkki
APPLICANT: Pasqualini, Renata
TITLE OF INVENTION: Structural Mimics of RGD-Binding Sites
NUMBER SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 8;
                                                                                                                                                                  ADDRESSER: Campbell & Flores LiP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                         COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/09/079,432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 23; DB 2;
Pred. No. 3e+05;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 1794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/520,535
FILING DATE: 28-AUG-1995
ATTORNEY/AGENT INFORMATION:
                  Sequence 3, Application US/09079432
Patent No. 5955572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50.0%;
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Best Local Similarity 37.3%,
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TOPOLOGY: circular
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1 CWDDGLMC 8
                                                              GENERAL INFORMATION:
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US-09-258-754-33
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        US-09-079-432-3
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geguence 214, Application US/09258754

general No. 6174687

GENERAL INFORMATION:
APPLICANT: Rueslahti, Erkki
APPLICANT: Rajotte, Daniel
TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
TITLE OF INVENTION: Membrane Dipeptidase
FILE REFERENCE: P-LJ 3443

CURRENT APPLICATION NUMBER: US/09/226

CURRENT APPLICATION NUMBER: 09/042,107

EARLIER FILING DATE: 1998-03-13

NUMBER OF SEQ ID NOS: 452

SOFTWARE: PATCHILING UNC: 2.0

SEQ ID NO 214

LENGTH: B

LENGTH: B

LENGTH: B

LENGTH: B
                                                                                                                                                                                                                                                                                      Sequence 42, Application US/09258754
; Sequence 42, Application US/09258754
; Patent No. 6174667
; GENERAL INFORMATION:
    APPLICANT: Rosalahti, Erkki
    APPLICANT: Rajotte, Daniel
    TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
    TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
    TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
    TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
    TITLE OF INVENTION: Wembrane Dipeptidase
    TURENT PILLIANION NUMBER: US/09/258,754
    CURRENT PILLING DATE: 1999-02-26
    EARLIER FILLING DATE: 1999-03-13
    NUMBER OF SEQ ID NOS: 452
    SOFTWARE: Patentin Ver. 2.0
    SEQ ID NO 42
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Length 8;
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Pred. No. 3e+05;
Score 23; DB 3;
Pred. No. 3e+05;
); Mismatches
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                                                                                        RESULT 13
US-09-042-107-33
IS-QUADICATION US/09042107
FALCAUT NO. 633-287
FALCAUT: Ruoslahti, Erkki
APPLICANT: Ruoslahti, Erkki
TITLE OF INVENTION: Molecules that Home to Various Selected Organs or TITLE OF INVENTION: Tissues
FILLE REPERENCE: P-Lu 2882
CURRENT APPLICATION NUMBER: US/09/042,107
CURRENT FILLNG DATE: 1998-03-13
NUMBER OF SEQ ID NOS: 436
SOFTWARE: PatentIn Ver. 2.0
ELENGTH: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-042-107-42

| Sequence 42, Application US/09042107
| Sequence 42, Application US/09042107
| Patent No. 6222287
| GENERAL INFORMATION:
| APPLICANT: Rooslahti, Erkki
| APPLICANT: Rosalahti, Renata
| TITLE OF INVENTION: Molecules that Home to Various Selected Organs or TITLE OF INVENTION: Molecules that Home to Various Selected Organs or TITLE OF INVENTION: Molecules that Home to Various Selected Organs or TITLE OF INVENTION: MOBER: US/09/042,107
| CURRENT APPLICATION NUMBER: US/09/042,107
| WOMBER OF SEQ ID NOS: 436
| SOFTWARE: PatentIn Ver: 2.0
| SEQ ID NO 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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CHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-042-107-33
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50.0%; Pred. No. 3e+05;
tive 1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 50.0
Matches 4; Conservative
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1 CFKSTLLC 8
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Best Local Similarity
Matches 4; Conserv
CNEESLIC
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US-09-042-107-214
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APPLICANT: Ruoslahti, Erkki
APPLICANT: Pasqualini, Renata
TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
TITLE OF INVENTION: Tissues
FILE REPERENCE: P-LJ 2892
CURRENT PILITON NUMBER: US/09/042,107
CURRENT FILID NOS: 436
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 214
LENGTH: 8
                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-042-107-214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
                                                                                                                                                                                                                                                                                                                                                                                               Query Match 50.0%; Score 23; DB 3; Length 8; Best Local Similarity 37.5%; Pred. No. 3e+05; Matches 3; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search completed: September 5, 2004, 10:40:46 Job time: 20 secs
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ORGANISM: Artificial Sequence
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1 CFKSTLLC 8
                                                                                                                                                                                                                                                                                                         FEATURE:
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OM protein - protein search, using sw model

September 5, 2004, 10:44:49; Search time 22 Seconds (without alignments) 48.096 Million cell updates/sec Run on:

US-09-761-636A-7 Title: Perfect score:

61 1 CISVPLTSVPC 11 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 segs, 96191526 residues Searched:

Total number of hits satisfying chosen parameters:

1327

seq length: 0 seq length: 11 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 78:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Gallbladder etone	+		hypotherical prote	205K excantigen	Iq beavy chain C r	T-cell recentor be	gamma-interferon-i	T-cell recentor be	metallothionein-A	118K stomach cance	תמי הובלה עה באל מן	nolvaalacturonase	vitellogenin 190k			tachykinin II - mi	1 5	Deptide-N4-(N-acet	Id H chain V-D-1 r	stathmin - mouse (-cell rece	major profein anti			•	adinokinetio homo		_
SUMMARIES	ID	77	₹	A60521	C39191	G33098	C39111	PH0944	S21727	PH0929	I51049	A60356	PT0247	S62880	A61622	PH0926	A32195	ECLQ2M	800616	B59272	PH1584	PN0042	PH0941	E60274	A35039	PC1316	966808	B49823	B44960	A33995
	DB	2	7	~	N	~	~	N	7	~	7	7	7	7	7	N	~	7	N	~	~	~	7	~	4	7	7	7	7	0
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	Score	22	20	19	18	17	17	17	17	17	16	16	16	16	16	16	16	16	16	15	15	15	15	14	14	14	14		14	14
	Result No.	Н	7	3	4	2	9	7	œ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	53

capsid protein VP-	fibroblast growth	neutral profeinage	orf dowstream to b	diuretic neuropent	seminal vesicle or	andiotensin-conver	hypertrehalosemic	hypertrehalosemic	hypotrehalosemic h	triacylglycerol ii	protein OA100052 -	alpha-dliadin 6Ha	hypothetical prote	bradokinin-notanti	pyrrologuinoline q
PL0184	A42057	A35180	B41983	A29477	I52974	XAVI6B	JC1416	809138	B33995	PC2171	PA0050	B61218	E86128	XASNBA	S58244
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23.0	23.0	23.0	23.0	23.0	23.0	23.0	23.0	23.0	23.0	23.0	23.0	23.0	23.0	23.0	23.0
14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

```
RESULT 1
D57789
gallbladder stone matrix protein, 14.5K - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Dete: 23-Feb-1996 #sequence_revision 23-Feb-1996 #text_change 23-Feb-1996
C;Accession: D57789
R;Binette, J.P.; Binette, M.B.
Submitted to the Protein Sequence Database, February 1996
A;Description: The proteins of gallbladder stones.
A;Accession: D57789
A;Accession: D57789
A;Reseiners: preliminary
A;Nelecule type: protein
A;Residues: 1-11 cBIN>
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0
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36.1%; Score 22; DB 2; Length 11;
Best Local Similarity 66.7%; Pred. No. 8.2e+02;
Matches 4; Conservative 0; Mismatches 2; Indels
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RESULT 2

MHC H2-L antigen - mouse (fragment)
C;5946
MHC H2-L antigen - mouse (fragment)
C;5pecies: Mus musculus (house mouse)
C;5pecies: Mus musculus (house mouse)
C;5atecies: Musculus (house mouse)
C;5atecies: Musculus (house mouse)
C;5atecies: 15546
R;Kimura, A.; Israel, A.; Le Bail, O.; Kourilsky, P.
C;1 44, 261-272, 1986
A;7itle: Detailed analysis of the mouse H-2Kb promoter: Enhancer-like sequences and their A;Reference number: 152778; MUID:86106202; PMID:3510743
A;Reference number: 152778; MUID:86106202; PMID:3510743
A;Reference number: Leste
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-6 <RES>
A;Residues: 1-6 <RES>
A;Residues: 1-6 <RES>

.; 0 0; Indels Query Match 32.8%; Score 20; DB 2; Le Best Local Similarity 100.0%; Pred. No. 2.8e+05; Matches 3; Conservative 0; Mismatches 0;

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Gaps

9 VPC 11 |||| 2 VPC 4 q à

RESULT 3 A60521

glycogen phosphorylase (EC 2.4.1.1), muscle - mullet (Liza ramada) (fragment)

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jg heavy chain C region - Pacific hagfish (fragment)
C;Species: Eptatretus stouti (Pacific hagfish)
C;Species: Boct-1991 #sequence_revision 18-Oct-1991 #text_change 16-Aug-1996
C;Accession: C39111
R;Varner, J; Neame, P; Litman, G.W.
R;Varner, J; Neame, P; Litman, G.W.
A;Title: A serum heterodimer from hagfish (Eptatretus stoutii) exhibits structural simil A;Reference number: A39111; MUID:91156684; PMID:2000382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C;Accession: PH0944
R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Mal, 174, 1467-1476, 1991
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergal A;Reference number: PH0891; MUID:92078857; PMID:1836012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gamma-interferon-induced protein IP-30 precursor - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
C;Date: 22-Nov-1993 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
R;Mc;Mcssesion: 821727
R;Mc;Mcssesion: 821727
Nature 356, 443-446, 1992
A;Title: HLA-A2 molecules in an antigen-processing mutant cell contain signal sequence-of-A;Reference number: S21727; MuID:92212461; PMID:1557127
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A,Molecule type: mRNA
A,Residues: 1-10 <GGL>
A,Experimental source: complete Freund's adjuvant-immunized lymph 1
A,Note: the authors translated the codon GAC for residue 9 as Glu
C,Keywords: T-cell receptor
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Pred. No. 5.6e+03;
0; Mismatches 2; Indels
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Pred. No. 5.6e+03;
0; Mismatches 1;
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A;Molecule type: protein
A;Residues: 1-10 «VAR»
C;Keywords: heterotetramer; immunoglobulin
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3; Conservative
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A.Molecule type: protein
A.Residues: 1-11 <WEI>
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J. Bacteriol. 173, 176-183, 1991
A.Title: Evidence that a novel tetracycline resistance gene found on two Bacteroides traces on mumber: A33191; MUID:91100280; PMID:1846135
A.Accession: C39191
A.Accession: C39191
A.Mostule: preliminary; not compared with conceptual translation
A.Mostules: 1-10 <SPE>
NyAlternate names: glycogen phosphorylase b (5)Pecies: Liza ramada (5)Pecies: Liza ramada (5)Pate: 17-Apr-1993 #text_change 18-Aug-2003 (5)Pate: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2003 (5)Accession: A60521 (5)Accession: A60521 (6)Pecies (6)Pecies (7)Pecies (
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C;Species: Plasmodium falciparum
C;Adcession: 933098
R;Nichols, J.H.; Hager, L.P.
Submitted to the Protein Sequence Database, May 1990
A;Reference number: A33098
A;Reference number: A33098
A;Reference protein: G30098
A;Re
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Pred. No. 3.8e+03;
1; Mismatches 2; Indels
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31.1%; Score 19; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 57.1%;
Matches 4; Conservative
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Best Local Similarity 66.7
Matches 4; Conservative
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A;Cross-references: GB:M37699
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3 LDVPTAAV 10

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2 VPLXLV 7

RESULT 6

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Ig heavy chain CRD3 region (clone 2-106A) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens
C;Accession: PT0247
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and j
A;Reference number: PT0222; MUID:91108337; PMID:1899102
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C;Species: Lymantria dispar (gypsy moth)
C;Date: 21-0ul-1995 #sequence_revision 28-Jul-1995 #text_change 15-Oct-1999
C;Accesion: A61622
R;Hiremath, S.; Eshita, S.
Insect Biochem. Mol. Biol. 22, 605-611, 1992
A;Title: Purification and characterization of vitellogenin from the gypsy moth, Lymantri
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C;Species: Aspergillus sp.
C;Species: Aspergillus sp.
C;Dacte: 28-0ct-1996 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
C;Accession: S62880
R;Stratilova, E.; Dzurova, M.; Markovic, O.; Joernvall, H.
FEBS Lett. 382, 164-166, 1996
A;Title: An essential tyrosine residue of Aspergillus polygalacturonase.
A;Reference number: S62880; MUID:96196586; PMID:8612742
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Best Local Similarity 100.0%; Pred. No. 8 46+03;
Matches 3; Conservative 0; Mismatches 0;
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A;Residues: 1-10 <STR>
C;Keywords: glycosidase; hydrolase
F;4/Active site: Tyr #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Keywords: egg yolk; hemolymph
                                                                                                                                                                                                                                                                                                                                                              A,Status: preliminary
A,Molecule type: protein
A,Residues: 1-10 <HIR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 SVPLTS 8
                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-9 < YAM>
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RESULT 12
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                       C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C;Accession: PH0929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          m
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A;Title: Western blotting analysis for malignant lymphoma and stomach cancer antigens
A;Reference number: A60356; MUID:90216080; PMID:2323853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rainbow trout (Oncorhyncus mykiss)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Oncorhynchus mykiss (rainbow trout)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C;Accession: IS1049
Eur. J. Blochem. 230, 344-349, 1995
A;Title: Structural and functional analysis of the rainbow trout (Oncorhynce A;Reference number: IS1049; MUID:95324545; PMID:7601121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          118K stomach cancer antigen - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 17-Mar-1999
C;Accession: A60356
                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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     T-cell receptor beta chain V-D-J region (clone 15) - rat (fragment)
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                                                                                                                                                                                                                                                                                                                                                                                                            3; Indels
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                                                                                                                                                                                                                           A;Molecule type: mRNA
A;Residues: 1-11 <GOL>
A;Experimental source: concanavalin A-activated lymphoblast
C;Keywords: T-cell receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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57.1%;
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Best Local Similarity 57.1
Matches 4; Conservative
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Best Local Similarity 50.0°
Matches 3, Conservative
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Best Local Similarity
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A Residues: 1-9 <SHI>
C Keywords: glycoprotein
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IPLKPV 6
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RESULT 15
PH0926
C1-cell receptor beta chain V-D-J region (isolate 12) - rat (fragment)
C1-cell receptor beta chain V-D-J region (isolate 12) - rat (fragment)
C1-cell receptor beta chain V-D-J region (isolate 12) - rat (fragment)
C1-cell receptor Battus norvegicus (Norway rat)
C1-cell receptor Battus norvegicus (Norway rat)
C1-cession: PH0926
C2-Accession: PH0926
A-Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allerging A-Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allerging A-Molecule type: mRNA
A-
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5 PLT 7
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2 PLT 4
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Search completed: September 5, 2004, 10:48:24 Job time: 23 secs

1 CASRP 5

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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                  Copyright
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OM protein - protein search, using sw model

September 5, 2004, 10:40:49; Search time 15 Seconds (without alignments) 38.185 Million cell updates/sec Run on:

US-09-761-636A-7 61 1 CISVPLTSVPC 11 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 seqs, 52070155 residues Searched:

441 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 11

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt 42:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	P82654 hoplobatrac	651		bos ta	homo	conns	locust	P14595 tabanus atr	P04549 periplaneta				P01022 bothrops ja	carausiu		P30423 bothrops in		P01021 agkistrodon	P55173 pseudomonas			P05487 conus stria	P30422 bothrops in		_	P80337 ovis aries	P81012 schizaphis	_	P83455 pachymedusa	P82157 cydia pomon	10 fusari	0	20 penaeu
SUMMARIES	;	er er	TIN4 HOPTI	1 1	COW2_CONPU		UPA4 HUMAN	CXL1_CONMR	LPK2_LOCMI	_	HTF2_PERAM	UPAA_HUMAN	DNF1_LOCMI	YBFR_AZOVI	BPP2_BOTJA	HTF2_CARMO	HTF_TABAT	BPP3_BOTIN	BPP4_BOTIN	BPPB_AGKHA	POOC PSEFL	EI01_LITRU	UPA1_HUMAN	CONO_CONST	BPP2_BOTIN	BPP_VIPAS	COXH ONCMY	COXO_SHEEP	ESTA_SCHGA	NS1_MYCTU	- 1	- 1	FUSS_FUSSO	- 1	FAR5_PENMO
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Tigerinin-1.
Hoplobatrachus tigerinus (Indian bull frog) (Rana tigerina).
Hoplobatrachus tigerinus (Indian bull frog) (Rana tigerina).
Amphibia: Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae;
Hoplobatrachus.
NCBI_TaxID=103373;

10.0T.1 HOPTI STANDARD; PRT; 11 AA. P82651; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 15-MAR-2004 (Rel. 43, Last annotation update)

RESULT 2 TIN1 HOPTI AC P82651 DT 16-OCT DT 15-MAR DE TIGERI OS HOPLO OC BUKATY OC BUKATY OC AMPHID OC AMPHID OC NOBL OX NCBL RP [1]

[1] -SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND DISULFIDE BONDS. TISSUE=Skin secretion;

P80159 treponema h P42995 bufo regula P24047 stromogneute P16224 locusta mig P30094 homo sapien P31031 proteus vul P23210 herpes simp P10420 mytilus edu P42984 leptinotars P82618 periplaneta P80975 thumus obe P43172 ascaris suu
9 1 FLA2 TREHY 9 1 OXYT_BUFRE 9 1 SAP STOVA 10 1 TKL2 LOCMI 10 1 UPA8 HUMAN 11 1 T221 PROVU 6 1 VP19 HSVIK 7 1 CARP_MYTED 7 1 MNP1 LEPDE 8 1 PPR3 PERAM 9 1 COXE_THUOB 9 1 COXE_THUOB 9 1 FAR9_ASCSU
19.7 119.7 119.7 119.7 118.0 118.0 118.0
4 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8

ALIGNMENTS

ESU TN4	RESULT 1 TIN4 HOPTI											
	TIN4 HOPTI	STAN	STANDARD;		PRT;	11	11 AA.					
	P82654;											
	16-OCT-2001			Created	~							
	16-OCT-2001			st se	Last sequence update)	pdat	(e)					
	10-OCT-2003	(Rel. 4)	42, Las	st an	Last annotation update)	pdn	(ate)					
	Tigerinin-4.					•						
	Hoplobatrachus tigerinus (Indian bull frog) (Rana tigerina).	us tige	rinus	(Ind	ian bull	fro	(6)	Rana	Ligerin	, (at		
20	Eukaryota; Metazoa; Chordata; Craniata; Vertehrata: Enteleostomi	etazoa;	Chorc	data;	Craniat	A : V	erte	brat	A Ente	a taca		
ဗ	Amphibia, Batrachia, Anura, Neobatrachia: Ranoidea: Panidae.	trachia	: Ann	ra: N	eobatrac	hia:	Ran	oide	A Ranio	. ee	1	
SC	Hoplobatrachus.	us.						1	7	,		
	NCBI TaxID=103373;	03373;										
RN	[1]	•										
RP	SEQUENCE, FUR	NCTION,	MASS	SPEC	TROMETRY	AN	Id d	SULF	FUNCTION, MASS SPECTROMETRY, AND DISULFIDE BONDS.	8		
RC	TISSUE=Skin secretion;	secretion	; dc									
RX	PubMed=11031261;	261;										
RA	Purna Sai K., Jaganadham M.V., Vairamani M., Raiu N.P.	, Jagan	adham	Μ. V.	, Vairam	ani	Σ	Raju	d. N			
RA	Devi A.S., Nagaraj R., Sitaram N.;	agaraj 1	R., Si	itara	Z							
	"Tigerinins:	novel	antimi	icrob	ial pept	ides	fro	m th	e Indian	frod	Rana	
	tigerina.";				1					6		
RI.	J. Biol. Chem. 276:2701-2707(2001),	n. 276:	2701-2	2707 (2001),							
g	-! - FUNCTION: Antibacterial activity against B subtilis. E coli	: Antiba	acteri	ial a	ctivity	agai	nst	B. Su	btilis.	E 00	_	
	S.aureus, M.luteus, P.putida and	, M. lute	eus, E	P. put	ida and	S.ce	S.cerevisiae	Siae		}	•	
	-1- SUBCELLULAR LOCATION: Secreted.	LAR LOCI	ATION:	Sec	reted.	1	! !	3				
	-!- TISSUE SPECIFICITY: Skin.	PECIFIC	TY: S	3kin.								
	-!- MASS SPEC	TROMETI	RY: MR	V=124	SPECTROMETRY: MW=1247; METHOD=MALDI.	D=MA	LDI.					
	Н-	fense pe	eptide	; Ant	tibiotic							
F.	DISULFID	е	11									
	SEQUENCE 11	11 AA; 1	1248 MW;		117D8EFD37605DCB CRC64;	3760	SDCB	CRC	64;			
ğ	Query Match		37.78;		Score 23; DB 1;	Ω.	д Т		Length 11:			
Ser	Best Local Similarity Matches	larity 50.	50.08;	·	Pred. No. 1.8e+02;	1,04	8e+0;		1000		į	(
	5	10000	}	4	dillo Tio	נכוום	۵		Tinera	•	caps	; 0
	1 CISVPL	7PL 6										
	3 CYAIPL	[PL 8										

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methylguanine-DNA methyltransferase) (Fragment)
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UPA4_HUMAN
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01-DEC-1992 (Rel. 24, Last sequence update)
01-DEC-1992 (Rel. 34, Last annotation update)
01-CCT-1996 (Rel. 34, Last annotation update)
Methylated-DNA--protein-cysteine methyltransferase (EC 2.1.1.63) (6-0-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
STRAIN=Clipperton Island; TISSUE-Venom;
MEDLINE=99388839; PubMed=10461743;
Jacobsen R.B., Jimenez E.C., De la Cruz R.G.C., Gray W.R., Cruz L.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Olivera B.M.;
"A novel D-leucine-containing Conus peptide: diverse conformational dynamics in the contryphan family.";
"J. Pept. Res. 54:39-39 (1999).
-! SUBCELLULAR LOCATION: Secreted.
-! TISSUE SPECTROMETRY: Expressed by the venom duct.
-! MASS SPECTROMETRY: WW-888.4; METHOD-LSIMS.
-! SIMILARITY: Belongs to the contryphan family.
TOXIN; Hydroxylation; D-amino acid.
DISULFID.
                          Purna Sai K., Jaganadham M.V., Vairamani M., Raju N.P.,
Devi A.S., Nagaraj R., Sitaram N.;
"Tigerinins: novel antimicrobial peptides from the Indian frog Rana
                                                                                                            J. Biol. Chem. 276:2701-2707(2001).
--- FUNCTION: Antibacterial activity against B.subtilis, E.coli, S.aureus, M.luteus, P.putida and S.cerevisiae.
--- SUBCELLULAR LOCATION: Secreted.
--- TISSUE SPECIFICITY: Skin.
--- MASS SPECIFROMETRY: MW=1342; METHOD=MALDI.
--- Amphibian defense peptide; Antibiotic; Fungicide; Amidation.
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                                                                                                                                                                                                                                                                                                                                               Score 19, DB 1; Length 11;
Pred. No. 9.7e+02;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
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                                                                                                                                                                                                                                                                                   AMIDATION.
A2087DC960476056 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 AA; 890 MW; 75A367672732CEB8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conus purpurascens (Purple cone).
                                                                                                                                                                                                                                                                                       MOD_RES 11 11 SEQUENCE 11 AA; 1344 MW;
                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 33.3%;
Matches 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 40...
2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            | :|:
CTMIPI 7
                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CISVPL 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CVLLP 6
           PubMed=11031261;
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ID MGMT BOVIN
AC P29177;
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                                                                                               tigerina."
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SEQUENCE
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COW2_CONPU
ID _COW2_CC
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-!- SIMILARITY: WITH SEGMENTS OF E.COLI ADA AND OGT METHYLTRANSFERASE WHICH ENCOMPASS THE ALKYL-ACCEPTOR RESIDUES.
INTERPRO; IPR01497; Methyltransf_1.
PROSITE; PS00374; MGMT; PARTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Plasma protein map: an update by microsequencing.";
Electrophoresis 13:707-714(1992).
--- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown protein is: 4.8, its MV is: 40.5 kda.
--- MISCELLANEOUS: This spot is on a position thought to be that of Zn-alpha-2 glycoprotein, but it does not correspond to that
       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALKYL GROUP ACCEPTOR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-APR-1993 (Rel. 25, Last sequence update)
15-MAR-2004 (Rel. 43, Last amnotation update)
Unknown protein from 2D-page of plasma (Spot 12) (Fragment).
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Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
Hochstrasser D.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 AA; 967 MW; 325171A720476047 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA repair; Transferase; Methyltransferase.
NON TER 1
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Bos taurus (Bovine).
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Best Local Similarity
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|3 IPILT-PC
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                                                                                       NCBI_TaxID=9913;
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us-09-761-636a-7.closed.rsp

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Local Similarity
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                                                                                                                                                                                                                                                                           AKH TABAT
P14595;
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             family."
                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                             Tabanus
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HTF2 PERAM
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Malaji R.A., Ohtake A., Sato K., Gopalakrishnakone P., Kini R.M.,
Seew K.T., Bay B.-H.;
"Lambda-conotoxins, a new family of conotoxins with unique disulfide
if pattern and protein folding isolation and characterization from the
ryenno of Conus marmoreus."

1. Diol. Chem. 275:39516-39522(2000).

1. FUNCTION: Inhibits the neuronal noradrenaline transporter.

2. SUBCELDULAR LOCATION: Secreted.

1. SUBCELDULAR LOCATION: Expressed by the venom duct.

2. INSS SPECTREOMERRY: MW=123-33, MW ERR=0.21; METHOD=Electrospray.

3. SIMILARITY: Belongs to the chi/lambda-conotoxin family.
                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Isolation, identification and synthesis of locustapyrokinin II from
Locusta migratoria, another member of the FXPRL-amide peptide
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                                                                                                                                                                                                                   Apogastropoda; Caenogastropoda; Ortnogastropoda;
Neogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
NCBI_TaxID=42752;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=94094539; PubMed=7903606;
Schoofs L., Holman G.M., Nachman R., Proost P., van Damme J.,
                                                                                                                                                                                                Conus marmoreus (Marble cone).
Eukaryota, Metazoa, Mollusca, Gastropoda, Orthogastropoda,
       Score 17; DB 1; Length 10;
Pred. No. 2e+03;
0; Mismatches 1; Indels
                               1; Indels
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        MOD_RES
        10
        10
        HYDROXYLATION.

        SEQUENCE
        11 AA;
        1226 MW;
        277AAC60B7232B58 CRC64;

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Pred. No. 3.4e+03;
                                                                                                                                                28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
Locustapyrokinin 2 (LOM-PK-2) (FXPRL-amide)
Locusta migratoria (Migratory locust)
                                                                                                                                  11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26.2%; Scc...
100.0%; Pred. No. 5...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 AA.
                                                                                                                                                                                                                                                                  SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
    27.9%;
                           4; Conservative
                                                                                                                              STANDARD;
                                                                                                                                                                                      Lambda-conotoxin CMrVIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                               4 VPLTS 8
                                                                      2 VPNTS 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Brain;
                                                                                                                             CXL1 CONMR
P58807;
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P41488;
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                       Matches
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Comp. Biochem. Physiol. 106C:103-109(1993).
-!- FUNCTION: Mediates visceral muscle contractile activity (myotropic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Tabanomorpha; Tabanidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=90046758; PubMed=2813385;
Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Nachman R.J.,
Vogel V.W., Zhang Y.-S., Hayes D.K.;
Vogel V.W., Zhang Y.-S.,
Varinary structure of two neuropeptide hormones with adipokinetic and hypotrephalosemic activity isolated from the corpora cardiaca of horse Proc. Natl. Acad. Sci. U.S.A. 86:8161-8164 (1989).

-I-FUNCTION: This hormone, released from cells in the corpora cardiaca after the beginning of flight, causes release of diglycerides from the fat body and then stimulates the flight muscles to use these diglycerides as an energy source.
                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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01-FEB-1994 (Rel. 28, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Adipokinetic hormone (AKH) (Dipteran corpora cardiaca factor I)
(DCC I).
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InterPro; IPR002047; AKH.
PROSTIE; PS00256; AKH; 1.
Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.
MOD RES

#MOD RES

#MIDATION: AMIDATION CARBOXYLIC ACID.
SEQUENCE 8 AA; 949 MW; 86786711A9D1A73 CRC64;
                                                                                                                                                                                                                                                                                                         Length 10;
                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23.0%; Score 14; DB 1; Length 8; 60.0%; Pred. No. 1.4e+05; Live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                10 10 AMIDATION.
10 AA; 1145 MW; CFAF4271A9D1B772 CRC64;
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8 AA; 949 MW; 86786771A9D1A736 CRC64;
                                                                                                                                                                                                                                                                                              24.6%; Score 15; DB 1; Le
100.0%; Pred. No. 4.7e+03;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 AA.
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13-AUG-1987 (Rel. 05, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tabanus atratus (Horse fly).
                                                                                                                                                                                                                                                                                                                                                         3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Conservative
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                                                                                                                                                                                                                                                                                                                       Best Local Similarity
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UPAA_HUMAN
ID UPAA_HUMAN
AC P30096;
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C SPECIES—B. Orientalis, TISSUB=Corpora cardiaca;

XX Gaede G., Rinehart K.L. Ur.;

A Gaede G., Rinehart K.L. Ur.;

T "Primary structures of hypertrehalosaemic neuropeptides isolated from the corpora cardiaca of the cockroaches Leucophaea maderae, for corpora cardiaca of the cockroaches Leucophaea maderae, and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombardment mass spectroometry.";

E in Chem. Hoppe-Seyler 371:345-34(1990).

E i.- FUNCTION: Hypertrehalosaemic factors are neuropeptides that elevate the level of trehalose in the hemolymph (trehalose is the major carbohydrate in the hemolymph of insects).

C i.- SUBCELLULAR LOCATION: Secreted.

NR PIR: BA4960: B44860.
                                                                                                                                                                                                                                                                                                                                                              MEDLINE-8429H79; PubMed-6591205;
Scarborough R.M., Jamieson G.C., Kalish F., Kramer S.J., McEnroe G.A.,
Miller C.A., Schooley D.A.;
"Isolation and primary structure of two peptides with
cardioacceleratory and hyperglycemic activity from the corpora
cardioac of Periplaneta americana.";
Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PSPECIES-1. decemlineata; TISSUB=Corpora cardiaca;
MEDLINE=90160053; PubMed=2576128;
Gaede G., Kalinar R.,
"The metabolic neuropeptides of the corpus cardiacum from the potato
beetle and the American cockroach are identical.";
01-FEB-1994 (Rel. 28, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypertrehalosaemic factor II (Neuropeptide M-II) (Periplanetin CC-2)
(PeA-CAH-II) (LeD-CC-II) (Hypertrehalosaemic neuropeptide II).
Leptinotarsa decemlineata (Colorado potato beetle), and
Blatta orientalis (Oriental cockroach).
Bukaryota; Metazoa; Arthopoda; Hexapoda; Insecta; Pterygota;
Neoptera; Orthoperoidea; Dictyoptera; Blattaria; Blattoidea;
                                                                                                                                                                                                                                                              Rinehart K.L. Jr.; "Striphurach neuropeptides assigned by fast atom "Structures of two cockroach neuropeptides assigned by fast atom bombardment mass spectrometry."; Biochem. Biophys. Res. Commun. 124:350-358(1984).
                                                                                                                                                                                                         SPECIES=P.americana;
MEDLINE=85046530; PubMed=6548628;
Witten J.L., Schaffer M.H., O'Shea M., Cook J.C., Hemling M.E.,
Rinehart K.L. Jr.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00226; AKH; 1.
Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
Pyrrolidone Carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 14; DB 1; Length 8;
Pred. No. 1.4e+05;
Nismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AMIDATION.
86745771A9D1A736 CRC64;
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                                                                                                                                                   Blattidae, Periplaneta.
NCBI_TaxID=6978, 7539, 6976;
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8 AA; 1006 MW;
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                                                                                                                                                                                                                                                                                                                                                          SPECIES=P.americana;
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PIR; S08996; S08996
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Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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TISSUE-Suboesophageal ganglion, and Thoracic ganglion;
XX MEDLINE-88077077; PubMed=3689410;
XX Proux J.P., Miller C.A., Li J.P., Carney R.L., Girardie A.,
XA Delaage M., Schooley D.A.;
XI Delaage M., Schooley D.A.;
XI Locusta migratoria.";
XI LOCUSTA MONOMER RES. COMMUN. 149:180-186(1987).
XI LOCUSTA MONOMER (F.) and homodimer (F2); disulfide-linked.
XI SIMILARITY: Belongs to the vasopressin/oxytocin family.
XI RIAPPOPLY: AND WINTHOPHYD.
XI INTERPO: IPRO00961; Neurhyp_horm.
XI RESPOSSUES; NEURONESSIN/OXYTOCIN family.
XI RESPOSSUES; NEURONESSIN MUNICAL MONOMER.
XI NEURONESSIN NEUROPHYS.
XI NEUROSTER; PSO0264; NEUROPHYS.
XI NEURONESSIN MUNICAL MININTHOPHYS.
XI NEURONESSIN MUNICAL MUNICAL MININTHOPHYS.
XI NEURONESSIN MUNICAL MUNICAL MININTHOPHYS.
XI NEURONESSIN MUNICAL MUNICA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Plasma protein map: an update by microsequencing.";
Blectrophoresis 13:707-714(1992).
-!- MISCELLANEOUS: On the 2D-gel the determined pl of this unknown protein is: 7, its MW is: 12 kDa.
                                                                 01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
16-MAR-2004 (Rel. 43, Last annotation update)
16-MAR-2004 (Rel. 43, Last annotation update)
17-MAR-2004 (Rel. 43, Last annotation update)
18-MAR-2004 (Rel. 43, Last annotation update)
18-MAR-2004 (Fragment)
18-MAR-2004 (Rel. 43, Last annotation)
18
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Boveryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neopiera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;

Acridoidea; Acrididae; Oedipodinae; Locusta.
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F2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali
Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
Hochstrasser D.F.,
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INTERCHAIN (WITH C-1)
AMIDATION.
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01-AUG-1990 (Rel. 15, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-Corpressin (Diuretic neuropeptide F1/F2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 AA.
8 AA.
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MEDLINE=93092937; PubMed=1459097;
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P16339;
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SEQUENCE
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NCBI_TaxID=7022, 7024;
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HTF2 CARMO
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               STW BCCCCCRETTS
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01-FEB-1994 (Rel. 28, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Bradykinin-potentiating peptide 10B (Anglotensin-converting enzyme
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Bothrops jararaca (Jararaca).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;

Viperidae; Crotalinae; Bothrops.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
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MEDLINE=72118526; PubMed=4334402;
Ondetti M.A., Williams N.J., Sabo E.F., Pluscec J., Weaver E.R.,
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MEDLINE=92196129; PubMed=1549605;
Grossman M.J., Hinton S.M., Minak-Bernero V., Slaughter C.,
                                                                                                        1; Indels
                                                         Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23.0%; Score 14; DB 1; Length 9; 75.0%; Pred. No. 1.4e+05;
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9 AA; 976 MW; 56EB176EB451A057 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Unification of the ferritin family of proteins.", Proc. Natl. Acad. Sci. U.S.A. 89:2419-2423(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 AA; 947 MW; DF98B5A1B417776D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-1992 (Rel. 22, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein in bfr 3'region (Fragment).
                                               23.0%; Score 14; DB 1; I
40.0%; Pred. No. 1.4e+05;
iive 2; Mismatches 1;
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Best Local Similarity 75.00;
                                                                                                   2; Conservative
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(Rel. 22,
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                                                                         Local Similarity
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ID BPP2_BOTJA
AC P01022;
SEQUENCE
                                                 Query Match
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CARBOHYDRAIE-LINKAGE SITE.

SPECIES=C.morosus; TISSUE=Corpora cardiaca;

MEDLINE=93129188; PubMed=1482345;

Gaede G., Kellner R., Rinehart K.L. Jr., Proefke M.L.;

"A tryptophan-substituted member of the AKH/RPCH family isolated from a stick insect corpus cardiacum.";

Biochem. Biophys. Res. Commun. 189:1303-1309 (1992)

-! FUNCTION: Hypertrahalosaemic factors are neuropeptides that elevate the level of trehalose in the hemolymph (trehalose is the major carbohydrate in the hemolymph of insects).

-! SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=90253659; PubMed=2340112; Gaded G., Rinehart K.L. Jr.; Gramphaca C. Structures of hypertrehalosaemic neuropeptides isolated from the corpora cardiaca of the cockroaches Leucophaca maderae, Gromphadorhina portentosa, Blattella germanica and Blatta orientalis and of the strick insect Extacosoma tiaratum assigned by tandem fast atom bombardment mass spectrometry.
Angiotensin-converting enzyme inhibitors from the venom of Bothrops
                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUL-1989 (Rel. 11, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypertrehalosaemic factor II (HTF-II) (Hypertrehalosaemic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Extatosoma tiaratum (Stick insect).

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Orthopteroidea; Phasmatodea; Euphasmida; Phasmatoidea;
Heteronemiidae; Carausius.
                    jararaca. Isolation, elucidation of structure, and synthesis.";
Biochemistry 10:4033-4039(1971).
-!- FUNCTION: This peptide both inhibits the activity of the angiotensin-converting enzyme and enhances the action of bradykinin by inhibiting the kinases that inactivate it.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPECIES=C.morosus; TISSUE=Corpora cardiaca; MEDLINE=87157103; PubMed=3828078; Gaede G., Rinehart K.L. Jr.; "Primary structure of the hypertrehalosaemic factor II from the corpus cardiacum of the Indian stick insect, Carausius morosus, determined by fast atom bombardment mass spectrometry."; i. Eliol. Chem. Hoppe-Seyler 368:67-75(1987).
                                                                                                                                                                                                                                                                                                                  .
                                                                                                                                                                                                                                                Score 14; DB 1; Length 10; Pred. No. 7.1e+03; Indels
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-!- MASS SPECTROMETRY: MW=1308.61; METHOD=FAB.
-!- MILLARITY: Belongs to the AKH / HRTH / RPCH family.
PIR; JC1416, JC1416.
PIR; S09138; S09138.
                                                                                                                                                   PIR; A01255; XAVIGB.

Hypotensive agent; Pyrrolidone carboxylic acid.

MOD RES

1 1 PYRROLIDONE CARBOXYLIC PSEQÜENCE 10 AA; 1232 MW; 30C53546C7741773 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                stick insect), and
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                                                                                                                                                                                                                                                                                                              1; Mismatches
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TISSUE-COPPORA CARTIAGOS;

MEDILINE=9046758; PubMed=2813385;

A Jaffe H., Raina M.K., Riley C.T., Fraser B.A., Nachman R.J.,

A Jaffe H., Raina Y.-S., Hayee D.K.;

NOGEL V.W., Zhang Y.-S., Hayee D.K.;

Noper Structure of two neuropeptide hormones with adipokinetic and structure of two neuropeptide hormones with adipokinetic and represent activity isolated from the corpora cardiaca of horse RT flies (Diptera).";

Prince (Diptera).";

Proc. Natl. Acad. Sci. U.S.A. 86:8161-8164(1989).

Proc. Natl. Appertrehalosaemic factors are neuropeptides that elevate the level of trehalose in the hemolymph (trehalose is the major carboxydrate in the hemolymph of insects).

Subschillar Locarion: Secreted.

Subschillar Locarion: Secreted.

Subschillar Locarion: Portolidone carboxylic acid.

Neuropeptide; Amidation; Pyrrolidone carboxylic acid.

Neuropeptide; Amidation; Pyrrolidone carboxylic acid.

MOD. RES.

MAIDATION: Applation; Pyrrolidone Carboxylic ACID.
                                                                                                                                                                                                                                                                                                                                                                                                   01-JAN-1990 (Rel. 13, Created)
01-FBB-1994 (Rel. 28, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypertrehalosaemic factor (HOTH) (Dipteran corpora cardiaca factor II)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tabanus atratus (Horse fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Tabanomorpha; Tabanidae;
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InterPro; IPR002047; AKH.

PROSITE; PS00256; AKH; 1.

Neuropeptide; Amidation; Glycoprotein; Pyrrolidone carboxylic acid.

MOD RES 1 1 1 CLINKED (MAN) (PROBABLE).

MOD_RES 10 10 AMIDATION.

MOD_RES 10 10 AMIDATION.
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                                                                                                                                                            Score 14; DB 1; Length 10;
Pred. No. 7.1e+03;
0; Mismatches 2; Indels
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                                                                                                                                                                  Query Match 23.0%;
Best Local Similarity 60.0%;
Matches 3; Conservative
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Best Local Similarity 60.0
Matches 3; Conservative
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P14596;
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HTF TABAT
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Search completed: September 5, 2004, 10:46:52 Job time : 15 secs

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September 5, 2004, 10:43:34; Search time 58 Seconds (without alignments) 59.840 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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2: sp_bacteria:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

fp_plant:*
sp_rodent:*
sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*

sp_rvirus:*
sp_bacteriap:*

sp_archeap:*

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Score 21; DB 6; Length 11; Pred. No. 3.6e+03; 2; Mismatches 1; Indels

h 34.4%; Similarity 57.1%; 4; Conservative

Local Similarity

Query Match Best Loca Matches

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8 AA.

OGGMMS PRELIMINARY, PRT; QGGMMS; 01-MAR-2003 (TrEMBLrel. 23, Created)

RESULT 2 QBGMM5 ID QBGMP AC QBGMP DT 01-M3

9 31.1 10 8 Q9TKE1 Q9tke1 neofabre 9 31.1 10 8 Q9TKE4 G9TKE1 Q9tke1 neofabre 9 31.1 10 8 Q9TKE4 G9TKE4 G9TK	118 118 222 223 243	666666666666666666666666666666666666666	33 33 31 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	000000000000000000000000000000000000000	00000000000	09THW7 09TKE3 09TKE3 09THK6 09THK6 09TKE8	leptosi leptosi leptosi kunzea leptosi leptosi kunzea
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10 AA

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[1] — SEQUENCE FROM N.A. MEDLINE=82196891; PubMed=6281735; Donoghue D.J., Hunter T.; Donoghue D.J., Hunter T.; Pubmed of subcloning DNA fragments by restriction site reconstruction. Application to sequencing the amino-terminal region of the transforming gene of Gazdar murine sarcoma virus."; Nucleic Acids Res. 10:2549-2564(1982).
                                                                                                                                                                                                                                                                                                      Donoghue D.J., Hunter T.;
"Recombination junctions of variants of Moloney murine sarcom virus:
"Recombination junctions of variants of Moloney murine sarcom virus:
J. Virol. 45:607-617(1983).
BMBL; K03105; AAA46491.1; -
BMBL; R03105; AAA46491.1; -
SEQÜENCE 10 AA; 1062 MW; F9ECFCBEA771B5B1 CRC64;
                                                             01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Env-mos fusion protein (Fragment).
Moloney murine leukemia virus.
Viruses; Retroid viruses; Retroviridae; Gammaretrovirus.
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12.08%; Score 20; DB
Local Similarity 75.0%; Pred. No. 5e+0
les 3; Conservative 0; Mismatches
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                                                      (TrEMBLrel: 01,
                          PRELIMINARY;
                                                                                                                                        NCBI_TaxID=11801;
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01-NOV-1996
01-NOV-1996
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"Recombination junctions of variants of Moloney murine sarcom virus:
Generation and divergence of a mammalian transforming gene.";
J. Virol. 45:607-617(1983).
BEMBL; K03106; AAA46492.1; -.
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STRAIN=BM3; PLASMID=PXIH1207;
STRAIN=BM3; PLASMID=PXIH1207;
STRAIN=BM3; PLASMID=PXIH1207;
FKOLOGALI G.Y., Mindlin S.Z., Gorlenko Z.M., Yurieva O.V.,
Petrova M.A., Nikiforov V.G.;
"A young family of transposable adaptive DNA segments identified in the Acinetobacter genus."
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ250234; CAG80784.1; --
EMBL; AJ486856; CAD310781; --
GO; GO:0046821; C:extrachromosomal DNA; IEA.
                                                                                                                                                          STRAIN=EW3; PLASWID=pKLH207;
Kholodii G.Y., Yurieva O.V., Mindlin S.Z., Gorlenko Z.M.,
Wikiforov V.G.;
"pKLH2-like aberrant transposons and possible mechanisms of their
dissemination.";
                                                                            Bacteria; Protecbacteria; Gammaprotecbacteria; Pseudomonadales;
Moraxellaces; Acinetobacter.
NCBI_TaxID=106395;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 01, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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Pred. No. 5e+03;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        32.8%; Score 20; DB 2; Length 8; 80.0%; Pred. No. 1e+06; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Moloney murine leukemia virus.
Viruses; Retroid viruses; Retroviridae; Gammaretrovirus.
                                                                                                                                                                                                                              Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE 10 AA; 1081 MW; 7BECFCBEA771B5A4 CRC64;
    01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                             8 AA; 911 MW; 2D71B2D6C1A73774 CRC64;
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MEDLINE=83164305; Pubmed=6300424;
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75.0%;
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Best Local Similarity 75.03
Matches 3; Conservative
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                                 Transposase (Fragment)
                                                             Acinetobacter sp. BW3.
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Q85598;
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Matches
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Score 20; DB 15; Length 10; Pred. No. 5e+03;

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MEDLINE=81164305; PubMed=6300424;
Donoghue D.J., Hunter T.;
Donoghue D.J., Hunter T.;
Generation and divergence of a mammalian transforming gene.";
J. Virol. 45:607-617(1983).
BMBL; K03108; AAA46494.1; -.
BMBL; K03108; AAA46494.1; -.
SEQUENCE 10 AA; 1081 MW; 7BECFCBEA771B5A4 CRC64;
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                                           01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 19, Last annotation update)
Moloney murine sarcoma virus (Strain m1) env/mos 5' junction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32.8%; Score 20; DB 15; Length 10; 75.0%; Pred. No. 5e+03; Live 0; Mismatches 1; Indels
                                                                                                                                            (Fragment).
Moloney murine leukemia virus.
Viruses; Retroviridae; Gammaretrovirus.
NCBI_TaxID=11801;
10 AA.
PRT;
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Best Local Similarity 75.0'
Matches 3; Conservative
  PRELIMINARY;
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056140

STPC 7

us-09-761-636a-7.closed.rspt

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O'Brien M.M., Quinn C.J., Wilson P.G.,
"Molecular Systematics of the Leptospermum Suballiance (Myrtaceae).";
Aust. J. Bot. 48:0-0(2000).
EMBL; AF184670; ARF03840.1; -.
GO; GO:0009507; C:chloroplast; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          O'Brien M.M., Quinn C.J., Wilson P.G.;
"Molecular Systematics of the Leptospermum Suballiance (Myrtaceae).";
Aust. 48:0-0(2000).
EMBL; AF184666; AAF03838.1. ..
GO; GO:0009507; C:chloroplast; IEA.
                                                                                Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
Myrtales; Myrtaceae; Melaleuca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
Myrtales, Myrtaceae, Callistemon.
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Pred. No. 7.6e+03;
0; Mismatches 2; Indels
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10 AA; 1172 MW; 1DB12CA1B1B76440 CRC64;
           01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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66.7%; Pred. No. 7.6e+03;
live 0; Mismatches 2;
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66.7%;
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                                                        Melaleuca viridiflora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Callistemon polandii.
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                                                                                                                                NCBI_TaxID=106062;
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                                                                                                                                                               SEQUENCE FROM N.A.
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Best Local Similarity
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                         AtpB (Fragment).
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Q9TKG2
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MEDLINE-95047254; PubWed=7958782;
Constable A., Mollet B.;
"Isolation and characterisation of promoter regions from Streptococcus thermophilus.",
FEMS Microbiol. Lett. 122:85-90(1994).
BMBL; X78210; RAAS5045.1; -
NON_TER
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"Molecular Systematics of the Leptospermum Suballiance (Myrtaceae).";
Aust. J. Bot. 48:0-0(2000).
BMBL; AF184675; ARF03845.1; -
GO; GO:0009507; C:chloroplast; IEA.
                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, Myrtales, Myrtaceae, Agonis.
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Pred. No. 7.6e+03;
0; Mismatches 2; Indels
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Streptococcus.
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                                              Last sequence update)
Last annotation update)
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Last annotation update)
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01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
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                         01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-DEC-2001 (TrEMBLrel. 19,
STP6 protein (Fragment).
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66.78;
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01-MAY-2000 (TrEMBLrel. 13,
01-JUN-2003 (TrEMBLrel. 24,
                                                                                                          Streptococcus thermophilus.
PRELIMINARY;
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                                                                                                                                                       NCBI_TaxID=1308;
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RESULT 7 Q9TKF7

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Matches

RESULT 8

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Gaps

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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

0

Gaps

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SEQUENCE FROM N.A. Olinn C.J., Wilson P.G.; O'Brien M.M., Quinn C.J., Wilson P.G.; "Molecular Systematics of the Leptospermum Suballiance (Myrtaceae)."; Aust. J. Bot. 48:621-628(2000).
                                                                          SEQUENCE FROM N.A.
O'Brien M.M., Quinn C.J., Wilson P.G.;
"Molecular Systematics of the Leptospermum Suballiance (Myrtaceae).";
Aust. J. Bot. 48:0-0(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Eukaryota, Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots, rosids; Myrtales; Myrtaceae, Asteromyrtus.
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Pred. No. 7.6e+03;
0; Mismatches 2; Indels
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Heslewcod M., Quinn C.J.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AFI84679; AAF03849.2; -.
GO; GO:0009507; C:chloroplast; IEA.
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NON TER 10 10
SEQUENCE 10 AA; 1172 MW; 1DB12CA1B1B76440 CRC64;
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Last sequence update)
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Last annotation update)
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EMBL; AF184678; AAF03848.1; -.
GO; GO:0009507; C:chloroplast; IEA.
             Myrtales, Myrtaceae, Angasomyrtus
NCBI_TaxID=106032;
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66.7%;
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10 AA; 1172 MW;
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Best Local Similarity
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01-MAY-2000 (
01-JUN-2003 (
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Q9TKE0;
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O'Brien M.M., Quinn C.J., Wilson P.G.;
"Molecular Systematics of the Leptospermum Suballiance (Myrtaceae).";
"Malecular Systematics of the Leptospermum Suballiance (Myrtaceae).";
"Malect J. Bot. 48;0-0(2000).
BMBL, AF184672, AAF03842.1; -.
GO; GO:0009507; C:chloroplast; IEA.
                                                                                                                                                SEQUENCE FROM N.A.
O'Brien M.M., Quinn C.J., Wilson P.G.;
O'Brien M.M., Quinn C.J., Wilson P.G.;
"Molecular Systematics of the Leptospermum Suballiance (Myrtaceae).";
Aust. J. Bet. 48:0.2000).
BENBL; AF184682; AAF03852.1;
GO; GO:0009507; C:chloroplast; IEA.
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               Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
Myttales; Myttales; Homalospermum.
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
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Pred. No. 7.6e+03;
0; Mismatches 2; Indels
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Pred. No. 7.6e+03;
0; Mismatches 2; Indels
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NON TER 10 10
SEQUENCE 10 AA, 1172 MW; 1DB12CA1B1B76440 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Last annotation update)
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66.7%;
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Similarity 66.7%;
4; Conservative
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      Homalospermum firmum.
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Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
Matches 4; Conserv
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O9TKF4
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"Molecular Systematics of the Leptospermum Suballiance (Myrtaceae).";
Aust. J. Bot. 48:0-0(2000).
EMBL; AF184700; AAF03869.1;
GO; GO:0009507; C:chloroplast; IEA.
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O'Brien M.M., Quinn C.J., Wilson P.G.;

Wolecular Systematics of the Leptospermum Suballiance (Myrtaceae).";

Aust. J. Bot. 48.0-0(2000).

EMBL; AF184683; AAF03853.1; -.

GO; GO:0009507; C:chloroplast; IEA.
                                                                                     Chloroplast.
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; Nyttales; Myttales; Moefabricia.
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Chloroplast.

Enkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
Myrtales; Myrtaceae; Kunzea.

NCBI_TaxID=106041;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31.1%; Score 19; DB 8; Length 10; 66.7%; Pred. No. 7.6e+03; ttive 0; Mismatches 2; Indels
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NON TER 10 10
SEQUENCE 10 AA; 1172 MW; 1DB12CA1B1B76440 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 AA.
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                                                             Neofabricia sericisepala.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 4; Conserv
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SEQUENCE FROM N.A.
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AtpB (Fragment). ATPB.
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Search completed: September 5, 2004, 10:47:58 Job time : 60 secs

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0; Gaps

Score 19; DB B; Length 10; Pred. No. 7.6e+03; 0; Mismatches 2; Indels

h 31.1%; Similarity 66.7%; 4; Conservative (

Local Similarity

Best Loc Matches

Query Match

Chloroplast.

NON TER 10 10 SEQUENCE 10 As; 1172 MW; 1DB12CA1B1B76440 CRC64;

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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                Copyright
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- protein search, using sw model protein

5, 2004, 10:40:24; Search time 64 Seconds (without alignments) 48.563 Million cell updates/sec September Run on:

1 CISVPLTSVPC 11 US-09-761-636A-7 score: Sequence: Title: Perfect

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

348779 Total number of hits satisfying chosen parameters:

1586107 seqs, 282547505 residues

Searched:

seq length: 0 seq length: 11 Minimum DB Maximum DB Maximum

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

A Geneseq 29Jan04:* geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp2004s:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	ID	AAU04526	AAU04542	AAU04545	AAU04543	AAU04544	AAU04532	AAU04533	AAU04529	AAR58418	AAE34703	AAW12561	AAW12615	ABP47579	ABP47580	AAR77368	ABP47596	AAY41619	AAR58417	AAY26265	ABR56927	AAG73418	ABG64264	AAR96138	AAW82212	AAW46562
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de	Query	100.0	96.7	93.4	88.5	85.2	74.6	67.2		49.5	49.5	9	49.2	47.5	47.5	44.3	44.3	42.6	42.6	42.6		42.6	42.6	41.8	41.8	41.8
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ALIGNMENTS

AAU04526 standard; peptide; 11 AA. VEGF based monocyclic peptide 3. (first entry) 26-SEP-2001

Human; VEGF; vascular endothelial growth factor; angiogenesis; neovascularisation; lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic. Synthetic

 11 /note= "This bond cyclises the peptide" Location/Qualifiers Key Disulfide-bond WO200152875-A1.

26-JUL-2001

18-JAN-2001; 2001WO-US001533.

18-JAN-2000; 2000US-0176293P. 16-MAY-2000; 2000US-0204590P.

(LUDW-) LUDWIG INST CANCER RES.

Cendron A; Stacker S, Hughes RA, Achen MG,

WPI; 2001-442248/47.

Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine residues

Claim 49; Page 32; 102pp; English.

The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human VEGFD (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring betabeta carbon separation distances on opposite antiparallel strands of a

residues.

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peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with angiogenesis, concaveration or lymphangiogenesis in a mammal with a condition characterised by angiogenesis, neovascularisation or lymphangiogenesis, neovascularisation or lymphangiogenesis. The condition is diabetic retinopathy, psoriasis, arthropathy, corpered or accident, post-angioplasty restenosis, head, heat or cold trauma, substance-induced neovascularisation of the liver, excessive cremena, substance-induced neovascularisation of the liver, excessive commone-related angiogenic dysfunction, diabetes induced neovascular gequelae, hypertension induced neovascular sequelae, or chronic liver infection. The peptides are also used to modulate vascular permeability or brain. The peptides are used to induced by fund cavity, pleura, or brain. The peptides are used to induced by Oserlae and Lymphatic or brain. The peptides are used to induced by VEGF. Or bend of are also used in combination with an anti-inflammatory agent, to treat a continuation in peripheral activity induced by VEGF. Or -D and are also used in combination with an anti-inflammatory agent, to treat a chronic inflammation, especially rheumatoid arthritis, psoriasis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 61; DB 4; Length 11; 100.0%; Pred. No. 0.0016; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .11
/note= "This bond cyclises the peptide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU04542 standard; peptide; 11 AA.
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16-MAY-2000; 2000US-0204590P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diabetic retinopathy
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Matches
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to cyclisation are used to interfere with anglogenesis.

to cyclisation are used to interfere with anglogenesis.

covascularisation or lymphangiogenesis in a mammal with a condition characterised by anglogenesis, neovascularisation or lymphangiogenesis.

Conservation is diabetic retinopathy, psoriasis, arthropathy, hemangioma, vascularised malignant or benign tumour, post recovery cerebrovascular accident, post-angloplasty restenosis, head, hear or careama, substance-induced meovascularisation of the liver, excessive trauma, substance-induced neovascular sequelae, or chronic liver sequelae, hypertension induced neovascular sequelae, or chronic liver infection. The peptides are also used to modulate vascular permeability in a mammal (the mammal has a condition characterised by fluid corbination in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain. The peptides are used to inage blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are used to interfere with at least one biological activity induced by VEGF-C or -D and are also used in combination with an anti-inflammatory agent, to treat a chronic inflammation, especially rheumatoid arthritis, psoriasis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                    The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human vEGPD (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring beta-beta carbon separation distances on opposite antiparallel strands of a peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides, dimeric bloyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              neovascularisation, lymphangiogenesis, psoriasis, tumour, diabetes induced neovascular sequelae, rheumatoid arthritis, diabetic retinopathy, chronic inflammation, cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 59, DB 4; Length 11; Pred. No. 0.0034; 1; Mismatches 0; Indels

    11 .11
    /note= "This bond cyclises the peptide"

                                     Example 25; Page 47; 102pp; English.
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16-MAY-2000; 2000US-0204590P.
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Best Local Similarity 90.9
Matches 10; Conservative
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diabetic retinopathy
                                                                                                         Query Match
Best Local Similarity
Thes 9; Conserve
         WPI; 2001-442248/47,
                                                                                                       Sequence 11 AA;
                                                                                                                                                                                Disulfide-bond
                                                                                                                                                  26-SEP-2001
                                                                                                                                                                        Synthetic.
     Achen MG,
                      residues.
                                                                                                                                            AAU04543;
                                                                                                                                  RESULT 4
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The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human verses of vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring beta beta carbon separation distances on opposite antiparallel strands of a peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior cyclisation are used to interfere with angiogenesis, convascularisation or lymphangiogenesis, neovascularisation or lymphangiogenesis.

Convascularisation or lymphangiogenesis in a mammal with a condition is diabetic retinopathy, psoriasis, arthropathy, convascular accident, post-angioplasty restenosis, head, heat or cold crauma, substance-induced neovascularisation of the liver, excessive confection. The peptides are also used to modulate vascular permeability in a mammal (the mammal has a condition characterised by fluid accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain. The peptides are also used to indeptes and lymphatic vasculature. The monomeric and bicyclic peptides are used to interfere with at least one biological activity induced by vEGF, VEGF-C or -D and care also used in combination with an anti-inflammatory agent, to treat a chronic inflammation in peripherally, which an entivity are provided and converse and provided are also used to interfere with at least one biological activity induced by VEGF-C or -D and chronic inflammation in converse and privity induced by vEGF-C or -D and chronic inflammation and privity induced by vEGF-C or -D and chronic inflammation in peripherally, with an enti-inflammatic architecture.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       are also used in combination with an anti-inflammatory agent, to tree chronic inflammation, especially rheumatoid arthritis, psoriasis and diabetic retinopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human, VBGF, vascular endothelial growth factor, angiogenesis, neovascularisation; lymphangiogenesis; psoriasis; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88.5%; Score 54; DB 4; Length 11; 72.7%; Pred. No. 0.023;
                                                                                                                                                                                                                                                                                                                                                                                                                       Cendron A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 25; Page 47; 102pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                   Stacker S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU04544 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VEGF based monocyclic peptide 22.
                                                                                                                                                                                                                                                                                                                                     (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                             18-JAN-2001; 2001WO-US001533.
                                                                                                                                                                                                                                    18-JAN-2000; 2000US-0176293P.
                                                                                                                                                                                                                                                                     16-MAY-2000; 2000US-0204590P.
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nes 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CISVPLTSVPC 11
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1 CITIPLTSLPC 11
                                                                                                                                                                                                                                                                                                                                                                                                                   Hughes RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-442248/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 11 AA;
                  WO200152875-A1
                                                                                      26-JUL-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                Achen MG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   residues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU04544;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Loca
Matches
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              à
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EXXEXEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 reconstruction or lymphanglogenesis, a mammal with a condition characterised by angiogenesis, neovascularisation or lymphanglogenesis, neovascularised by angiogenesis, neovascularisation or lymphanglogenesis. The condition is diabetic retinopathy, psoriasis, arthropathy, recovery cerebrovascular accident, post-angioplasty restenosis, head, heat or cold frauma, substance-induced neovascularisation of the liver, excessive hormone-related angiogenic dysfunction, diabetes induced neovascular sequelae, nypertension induced neovascular sequelae, or chronic liver infection. The peptides are also used to modulate vascular permeability in a mammal (the mammal has a condition characterised by fluid accumulation in peripheral limps or in lungs, peritoneal cavity, pleura, or brain. The peptides are used to image blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are used to interfere with at least one biological activity induced by VEGF, VEGF-C or -D and are also used in combination with an anti-inflammatory agent, to treat a discrete control of the contro
                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human VEGFD (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring betabeta carbon separation distances on opposite antiparallel strands of a peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior rocyclistic action are used to interfere with angiogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                      Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ٠,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; VEGF; vascular endothelial growth factor; angiogenesis;
neovascularisation; lymphangiogenesis; psoriasis; tumour;
diabetes induced neovascular sequelae; rheumatoid arthritis;
diabetic retinopathy; chronic inflammation; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93.4%; Score 57; DB 4; Length 11; 81.8%; Pred. No. 0.0072; ive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "This bond cyclises the peptide"
                                                                              Cendron A;
                                                                                                                                                                                                                                                                                                                                                                                         Example 25; Page 47; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                          Stacker S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU04543 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VEGF based monocyclic peptide 21.
(LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CISVPLTSVPC 11
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                                                                          Hughes RA,
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Gaps

0;

0; Indels

VEGF based monocyclic peptide 10.

(first entry)

26-SEP-2001

AAU04532;

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The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human VEGPO (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring beta carbon separation distances on opposite antiparallel strands of a peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with angiogenesis. The condition or lymphangiogenesis in a mammal with a condition condition is diabetic retinopathy, psoriasis, arthropathy, cerebrovascular accident, post-angioplasty restenosis, head, heat or cold trauma, substance-induced neovascularisation of the liver, excessive correlated angiogenic dysfunction, diabetes induced neovascular sequelae, hypertension illuced neovascular sequelae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               infection. The peptides are also used to modulate vascular permeability in a mammal (the mammal has a condition characterised by fluid accomplation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain. The peptides are used to image blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are used to interfere with at least one biological activity induced by vEGF. VEGF-C or D and are also used in combination with an anti-inflammatory agent, to treat a chronic inflammation, especially rheumatoid arthritis, psoriasis and
diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic.
                                                                                                       Location/Qualifiers
1. .11
/note= "This bond cyclises the peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                    Cendron A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 25; Page 47; 102pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                      Stacker S,
                                                                                                                                                                                                                                                                                                                                                                                             (LUDW-) LUDWIG INST CANCER RES.
                                                                                                                                                                                                                                                                                                                            18-JAN-2000; 2000US-0176293P.
16-MAY-2000; 2000US-0204590P.
                                                                                                                                                                                                                                                                                   18-JAN-2001; 2001WO-US001533
                                                                                                                                                                                                                                                                                                                                                                                                                                      Hughes RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diabetic retinopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-442248/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 11 AA;
                                                                                                                                Disulfide-bond
                                                                                                                                                                                                  WO200152875-A1
                                                                                                                                                                                                                                          26-JUL-2001
                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                      Achen MG,
    88X88XEFFX8XBXBXBXBXBXBXBXBXBXBXBXBXBXBXBXBXBX8XBXBX8XBXBX8XXBX
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Score 52; DB 4; Length 11; pred. No. 0.049; 3; Mismatches 0; Indels
    85.2%;
      Query Match
Best Local Similarity
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1 CISVPLTSVPC 11 |||:|::||| CISLPISSVPC 11

Conservative

8;

Matches

à

AAU04532 standard; peptide; 10 AA. RESULT 6 AAU04532 ID AAU0

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Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine
                                                    growth factor; anglogenesis;
                                                           neovascularisation; lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic.

    10
/note= "This bond cyclises the peptide"

                                                                                                                                                                                                                                    Cendron A;
                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                    Stacker S,
                                                      endothelial
                                                                                                                                                                                                                     (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                           18-JAN-2000; 2000US-0176293P.
16-MAY-2000; 2000US-0204590P.
                                                                                                                                                                             .8-JAN-2001; 2001WO-US001533.
                                                                                                                                                                                                                                     Achen MG, Hughes RA,
                                                      Human; VEGF; vascular
                                                                                                                                                                                                                                                    WPI; 2001-442248/47
                                                                                                               Key
Disulfide-bond
                                                                                                                                              WO200152875-A1
                                                                                                                                                             26-JUL-2001.
                                                                                              Synthetic
                                                                                                                                                                                                                                                                                            residues.
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The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human CC whose 3-dimensional structure is modelled on the expose loop of human CC whose 1-dimensional structure is modelled by the invention relates to a method of producing a monomeric monocyclic peptide by a measuring beta-beta carbon separation distances on opposite antiparallel strands of a cyclising the peptide hop fragment from an exposed loop of a growth factor protein and cyclising the peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with angiogenesis, to cyclisation or lymphangiogenesis in a mammal with a condition of characterised by angiogenesis; neovascularisation or lymphangiogenesis. The condition is diabetic retinopathy, paoriasis, atthropathy, hear or cold creator accident, post-angioplasty restenosis, head, heat or cold creators underly accident, post-angioplasty restenosis, head, heat or cold crauma, substance-induced neovascular sequelae, or chromic liver, excessive condition induced neovascular sequelae, or chromic liver infaction induced neovascular sequelae, or chromic liver infaction induced neovascular sequelae, or chromic liver infaction induced neovascular sequelae. infection. The peptides are also used to modulate vascular permeability in a mammal (the mammal has a condition characterised by fluid accountiation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain. The peptides are used to image blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are used to interfere with at least one biological activity induced by VEGF. VEGF-C or D and are also used in combination with an anti-inflammatory agent, to treat a chronic inflammation, especially rheumatoid arthritis, psoriasis and diabetic retinopathy

Claim 49; Page 32; 102pp; English.

Sequence 10 AA;

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Gaps

. 0

Gaps 7 DB 4; Length 10; Indels .. 74.6%; Score 45.5; DB 90.9%; Pred. No. 0.52; cive 0; Mismatches Conservative Best Local Similarity 10; Query Match Matches

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to cyclisation are used to interfere with angiogenesis.

to cyclisation are used to interfere with angiogenesis.

covascularisation or lymphangiogenesis in a mammal with a condition

characterised by angiogenesis, neovascularisation or lymphangiogenesis.

The condition is diabetic retinopathy, psoriasis, arthropathy, the condition is diabetic retinopathy, psoriasis, arthropathy, that or cerebrowscular accident, post-angioplasty restenosis, head, heat or cold trauma, substance-induced neovascularisation of the liver, excessive hormone-related angiogenic dysfunction, diabetes induced neovascular sequelae, or chronic liver infection. The peptides are also used to modulate vascular permeability in a mammal (the mammal has a condition characterised by fluid corumnitation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain. The peptides are used to in lungs, peritoneal cavity, pleura, or brain. The peptides are used to induced by VEGF, VEGF-C or -D and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        whose 3-dimensional structure is modelled on the expose loop of human VBGPD (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a mesuring beta-beta carbon separation distences on opposite antiparallel strands of a peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human, VEGF, vascular endothelial growth factor; angiogenesis; neovascularisation; lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis;

    .9 // This bond cyclises the peptide"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diabetic retinopathy; chronic inflammation; cyclic.
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                                                                                                                                                                                                                                                      AAU04533 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VEGF based monocyclic peptide 11.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-JAN-2001; 2001WO-US001533.
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                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                CISVPL-SVPC 10
CISVPLTSVPC 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hughes RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-442248/47.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200152875-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                         AAU04533;
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                                                                                                                                                                                                         AAU(04533
LID AAU(04533
LID AAU(045333
LID AAU(045333
LID AAU(045454)
LID AAU(
                                                                                                                                                                           RESULT 7
   8
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Cendron A;

Stacker S,

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1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human VBGFD (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring beta carbon separation distances on opposite antiparallel strands of a peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidialing the cysteine residues. The monocyclic peptides, dimeric bicyclic peptides (comprishing 2 linked monocyclic peptides, dimeric bicyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with anglogenesis, no cyclisation or lymphangiogenesis in a mammal with a condition characterised by anglogenesis, neovascularisation or lymphangiogenesis. The condition is diabetic retinopathy, psoriagis, arthropathy, he manglomer, post-recovery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine
are also used in combination with an anti-inflammatory agent, to treat a chronic inflammation, especially rheumatoid arthritis, psoriasis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
                                                                                                                                          Gaps
                                                                                                                                        2
                                                                                                                                                                                                                                                                                                                                                                                                                            Human; VEGF; vascular endothelial growth factor; angiogenesis; neovascularisation; lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic.
                                                                                                    Score 41; DB 4; Length 9;
Pred. No. 1.4e+06;
0; Mismatches 0; Indels

    9 // This bond cyclises the peptide"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cendron A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 49; Page 32; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stacker S,
                                                                                                                                                                                                                                                                                           AAU04529 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                              VEGF based monocyclic peptide 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-JAN-2001; 2001WO-US001533.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-JAN-2000; 2000US-0176293P.
16-MAY-2000; 2000US-0204590P.
                                                                                                                   81.8%;
                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                   Query Match
Best Local Similarity 81.0
                                                                                                                                                                        1 CISVPLTSVPC 11
                                                                                                                                                                                                        σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hughes RA,
                                                                                                                                                                                                      1 CISVPL--VPC
                                   diabetic retinopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-442248/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disulfide-bond
                                                                   Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200152875-A1
                                                                                                                                                                                                                                                                                                                                                             26-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                             AAU04529;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Achen MG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              residues
                                                                                                                                                                                                                                                                           AAU04529
                                                                                                                                                                                                                                                           RESULT
                                                                                                                                                                                                                                                                                                             8 x 8 8 8 8
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cerebrovascular accident, post-angioplasty restenosis, head, heat or cold

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AARS8412-42 are overlapping 8-mer peptides of the binding domain of TSAR (Totally Synthetic Affinity Reagents) peptide TSAR (46.9-2 (AARS8411). These bind (partially) a monoclonal antibody, ie. anti-CEA (46 (anticarcinoembryonic antigen). TSAR peptides are generated using generic oligonucleotides (see AAQ70470-73 for examples). TSARs are concatenated heterofunctional proteins or peptides, comprising at least two functional regions - a binding domain with affinity for a ligand and a second effector peptide portion that is chemically or biologically active.They may further comprise a linker peptide between the 2 domains. The TSARs or
             hormone-related angiogenic dysfunction, diabetes induced neovascular sequelae, hypertension induced neovascular sequelae, or chronic liver infection. The peptides are also used to modulate vascular permeability in a mammal (the mammal limbs or in lungs, peritoneal cavity, pleura, or brain. The peptides are used to image blood vessels and lymphatic or brain. The monomeric and bicyclic peptides are used to interfere with at least one biological activity induced by VEGF. Or D and are also used in combination with an anti-inflammatory agent, to treat a chronic inflammation, especially rheumatoid arthritis, psoriasis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TSAR; totally synthetic affinity reagent; synthetic; binding domain; effector domain; concatenated heterofunctional protein; linker; direct, rapid; detection; screening; treatment; monoclonal antibody; MAb; C46; anti-carcinoembryonic antigen; anti-CRA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins comprising a
                                                                                                                                                                                                                                                                                                                  Gaps
trauma, substance-induced neovascularisation of the liver, excessive
                                                                                                                                                                                                                                                                                                                .,
                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                           4; Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Partial peptide 7 from TSAR C46.9-2 binding domain.
                                                                                                                                                                                                                                                                             DB 4; Le
                                                                                                                                                                                                                                                                           52.5%; Score 32; DB 100.0%; Pred. No. 1.4 iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 7.5; Page 108; 255pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  binding domain and an effector domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR58418 standard; protein; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93US-00013416.
93US-00176500.
94US-00189331.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                       Query Match 52.5
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1994-279739/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fowlkes DM;
                                                                                                                                                                                                      diabetic retinopathy
                                                                                                                                                                                                                                                                                                                                                  3 SVPLTSV 9
                                                                                                                                                                                                                                                                                                                                                                                       SVPLTSV 8
                                                                                                                                                                                                                                        Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9418318-A1
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31-JAN-1994;
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13-APR-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR58418;
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               a chemically or biologically active moiety, eg. metal ion, radioisotope, peptide, toxin or enzyme, to the specific target or on the cell. They can also replace the function of macromolecules eg. monoclonal or polyclonal antibodies and therefore circumvent the need for complex methods of hybridoma formation or in vivo antibody production. The TSARs are easily characterised and have designed activity allowing direct and rapid detection in a screening process. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid molecule comprising sequences encoding the CA125 protein, useful for diagnosing, preventing and/or treating cancer, e.g. ovarian, pancreatic, breast, endometrial or lung carcinomas.
comprising a TSAR binding domain can be used in vivo to deliver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a nucleic acid molecule encoding an ovarian cancer antigen, CA125. Nucleic acid molecules, vaccine and methods are useful for diagnosing, preventing and treating cancer, e.g. pancreatic, lung, ovarian, breast or endometrial carcinoma. The invention is useful in gene therapy and as vaccines. The present sequence is CA125/MUC16 Oglycosylation site
                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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0
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                                                                                                                                                                                              Score 30; DB 2; Length 8;
Pred. No. 1.4e+06;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49.2%; Score 30; DB 6; Length 9; 75.0%; Pred. No. 1.4e+06; rive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CA125; antigen; cancer; gene therapy; vaccine; MUC16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SLOK ) SLOAN KETTERING INST CANCER RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CA125/MUC16 O-glycosylation site #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 19; 70pp; English.
                                                                                                                                                                                                                                                                                                                                                                             AAE34703 standard; peptide; 9 AA.
                                                                                                                                                                                                 49.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-MAY-2002; 2002WO-US014768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-MAY-2001; 2001US-0290480P
                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Conservative
                                                                                                                                                                                                                                5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-129305/12.
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                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                                                                                                 1 CISVPLTS
                                                                                                                                                                                                                                                                                                CVSAPOTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200292836-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 9 AA;
                                                                                                                                                                   Sequence 8 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                             14-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-NOV-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lloyd KO,
                                                                                                                                                                                                                                                                                                                                                                                                               AAE34703;
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                                                                                                                                                                                                   Query Match
                                                                                                                                 field.)
                                                                                                                                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                               RESULT 10
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Core peptide; src homology region 2 binding peptide; SH2; cell growth; differentiation; regulation; receptor tyrosine kinase pathway; cancer; signal transduction pathway; non-insulin dependent diabetes; insulin-resistant diabetes.

SH2 binding peptide core sequence #21.

08-APR-1997 (first entry)

AAW12615;

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The sequences given in AAW12551-70 represent core peptides of an src homology region 2 (SH2) binding peptide which correspond to the formula: 27-x28-X x = any D- or L- amino acid; Z7 = phosphotyrosine or its isostere: 28 = asparagine or its isostere; the amino terminus is acylated, and the peptide is less than 14 residues in length, with the proviso that if Z7 is phosphotyrosine and Z8 is asparagine, then the peptide is not GDG27xZ8xPLLL. SH2 binding peptides containing these core peptides are used to treat of diagnose diseases associated with aberrant defects in receptor tyrosine kinase pathways, by partially blocking or cancer, a developmental or differentiation disease or insulin-resistant (or non-insulin dependent) diabetes
                                                                                                                                                     Core peptide; src homology region 2 binding peptide; SH2; cell growth; differentiation; regulation; receptor tyrosine kinase pathway; cancer; signal transduction pathway; non-insulin dependent diabetes; insulin-resistant diabetes.
                                                                                                                                                                                                                                                                                                           /note= "given in the patent as pl, no further details
given. May be intended to be phosphotyrosine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide(s) which bind to SH2 domains - are used to treat diseases associated with aberrant cell growth, differentiation or regulation associated with defects in receptor tyrosine kinase pathways.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Grove JR, Hart CP, Kim MH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 30; DB 2;
Pred. No. 1.9e+02
L; Mismatches
                                                                                                                     SH2 binding peptide core sequence #11.
                                                                                                                                                                                                                                                                 Location/Qualifiers
                            AAW12561 standard; peptide; 10 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gordon E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 8; Page 116; 203pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (AFFY-) AFFYMAX TECHNOLOGIES NV
                                                                                                                                                                                                                                                                                              /label= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                       96WO-US001544.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71.48;
                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DV, Gordeev MF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1996-371373/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Szardenings AK;
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                                                                                                                                                                                                                                                                Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                    31-JAN-1996;
                                                                                           08-APR-1997
                                                                                                                                                                                                                                                                                                                                                          WO9623813-A1
                                                                                                                                                                                                                                                                                                                                                                                        08-AUG-1996.
                                                                                                                                                                                                                                 Synthetic
                                                              AAW12561;
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RESULT 11
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Peptide(s) which bind to SH2 domains - are used to treat diseases associated with aberrant cell growth, differentiation or regulation associated with defects in receptor tyrosine kinase pathways.

Claim 13; Page 117; 203pp; English.

Kim MH;

Hart CP,

Grove JR,

Gordon E,

Gordeev MF,

Szardenings AK;

Patel DV,

WPI; 1996-371373/37.

(AFFY-) AFFYMAX TECHNOLOGIES NV.

96WO-US001544

31-JAN-1996; 38-AUG-1996

WO9623813-A1

Synthetic

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This sequence represents a core peptide of an src homology region 2 (SH2) binding peptide corresponding to the formula: Z7-X-Z8-X X = any D- or L- amino acid; Z7 = hosphotyrosine or its isostere; Z8 = asparagine or its isostere; the amino terminus is acylated, and the peptide is less than 14 isostere; the amino terminus is acylated, and the peptide is less than 14 is saparagine, then the peptide is not GDCZ7XZ8KPLLL. SH2 binding peptides containing this core peptide are used to treat of diagnose diseases associated with aberrant cell growth, differentiation or regulation which is associated with defects in receptor tyrosine kinase pathways, by partially blocking or inhibiting a cellular signal transduction pathway. The disease may be cancer, a developmental or differentiation disease or insulin-resistant (or non-insulin dependent)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps

    N. meningitidis LOS peptidic mimotope related peptide SEQ ID NO:155.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neisseria meningitidis; meningococcus; meningococcal; vaccine; LOS; lipooligosaccharide; monoclonal antibody; antibacterial; infection; antiinflammatory; meningococcal disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 30; DB 2; Length 11;
Pred. No. 2.1e+02;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABP47579 standard; peptide; 11 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5; Conservative
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CINVPFT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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Gaps

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Length 10;

1.9e+02;

AAW12615 standard; peptide; 11 AA.

RESULT 12
AAW12615
ID AAW12

CINVPFT

Voet

Neisseria meningitidis

Synthetic.

WO200228888-A2

11-APR-2002

(SMIK) SMITHKLINE BEECHAM BIOLOGICALS.

Letesson J,

WPI; 2002-479596/51.

03-OCT-2001; 2001WO-EP011409 03-OCT-2000; 2000GB-00024200 Claim 15; Page 43; 55pp; English.

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The present invention describes mimotopes (I) of a surface L3, 7, 9, of meningococcal lipopolysaccharides (LOS) of Neisseria meningitidis comprising a peptide peptide by screening a peptide library with a monoclonal antibody (MAD) like 4BE12C10, H44/24, H44/58, H44/70 or A44/78. (I) is antigenically cross-reactive with MAD. (I) have carbines. MAD is useful in the identification of (I). (I) or MAD are useful as a medicament, and also in the manufacture of a medicament for treating or preventing meningococcal disease. (I) and MAD are useful for treating or preventing from or susceptible to meningococcal disease treating or patient suffering from or susceptible to meningococcal disease. Or assay for meningococcal infection to detect antibodies against L3, 7, 9, LOS and to detect the presence of L3, 7, 9 immunotype meningococcus in a sample from a patient. ADN88481 and ABD47336 to ABD47754 crepresent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA encoding CAI resistance proteins - used in gene therapy, and for detecting CAI resistance in biological samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carboxyamido-triazole resistance; CAI; CAIR-1; cancer; gene therapy; Src homology 3; SH3 binding domain.
                                                                                                                                                                                  Novel mimotope of Neisseria meningitidis surface, for treating meningococcal disease, comprising a peptide epitope obtainable by screening peptide library with a specific monoclonal antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                          Poolman J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47.5%; Score 29; DB 5; Length 11; 36.4%; Pred. No. 3.1e+02; ive 2; Mismatches 5; Indels
                                                                                          Lobet Y, Mertens PY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                             (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR77368 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                    Claim 15; Page 43; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Liotta LA, Kim YS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95WO-US003610
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03-OCT-2000; 2000GB-00024200
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                                                                                             Letesson J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                            WPI; 2002-479596/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-MAR-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-SEP-1995.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR77368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes mimotopes (I) of a surface L3, 7, 9, of meningococcal lipopolysaccharides (LOS) of Neisseria meningitidis comprising a peptide epitope obtained by screening a peptide library with a monoclonal antibody (MAD) like 4BB12C10, H44/24, H44/58, H44/70 or H44/78. (I) is antigenically cross-reactive with MAD. (I) have cartiforerial and antihinflammatory activities, and can be used in vaccines. MAD is useful in the identification of (I). (I) or MAB are useful as a medicament, and also in the manufacture of a medicament for treating or preventing meningococcal disease. (I) and MAB are useful if treating or preventing from or susceptible to meningococcal disease by administering (I) or MAB to the patient. (I) is useful in a diagnostic by administering (I) or MAB to the patient. (I) is useful in a diagnostic assay for meningococcal infection to detect antibodies against L3, 7, 9, LOS and to detect the presence of L3, 7, 9 immunotype meningococcus in a sample from a patient. ABN88464 to ABN88487 and ABP47336 to ABP47754 cepresent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                     Voet P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N. meningitidis LOS peptidic mimotope related peptide SEQ ID NO:156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neisseria meningitidis; meningococcus; meningococcal; vaccine; LOS; lippoligosaccharide; monoclonal antibody; antibacterial; infection; antinflammatory; meningococcal disease.
                                                                                                                                                                                                                                                                                                                                                                                                               Novel mimotope of Neisseria meningitidis surface, for treating meningococcal disease, comprising a peptide epitope obtainable by screening peptide library with a specific monoclonal antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
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                                                                                                                                                                                                                                                                                                                       Poolman J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47.5%; Score 29; DB 5; Length 11; 27.3%; Pred. No. 3.1e+02; ive 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                     Lobet Y, Mertens PY,
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ABP47580 standard; peptide; 11 AA

RESULT 14 ABP47580 ID ABP4 XX

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3; Conservative 1 CISVPLTSVPC 11 | :::| | | | 1 CVTIPYRGTQC 11

Query Match Best Local Similarity Sequence 11 AA;

19-AUG-2002 (first entry)

ABP47580;

03-OCT-2001; 2001WO-EP011409.

Neisseria meningitidis

WO200228888-A2

11-APR-2002

0

Gaps

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Example 4; Page 40; 56pp; English.
8 X C C C C X 8
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CAIR-1 protein (AAR77365), responsible for CAI resistance in A2058 human melanoma cells, contains a unique proline-rich sequence which fulfills the consensus definition for Src homology 3 (SH3) binding proteins (AAR77366). 4 Unique versions (AAR77367-70) are present

Sequence 10 AA;

Gaps ; Query Match
44.3%; Score 27; DB 2; Length 10;
Best Local Similarity 62.5%; Pred. No. 6e+02;
Matches 5; Conservative 0; Mismatches 3; Indels

; 0

4 VPLTSVPC 11

ò Db

Search completed: September 5, 2004, 10:46:32 Job time : 66 secs

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Sequence 23, Appl
Sequence 24, Appl
Sequence 24, Appl
Sequence 25, Appl
Sequence 13, Appl
Sequence 11, Appl
Sequence 13, Appl
Sequence 332, App
Sequence 332, App
Sequence 156, Appl
Sequence 157, Appl
Sequence 156, Appl
Sequence 157, Appl
Sequence 158, Appl
Sequence 158, Appl
Sequence 158, Appl
Sequence 1521, Appl
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                                                                                                                                     (without alignments)
51.727 Million cell updates/sec
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| cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
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3: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
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18: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-761-636A-26

US-09-761-636A-24

US-09-761-636A-14

US-09-761-636A-13

US-09-761-636A-14

US-09-761-636A-14

US-09-761-636A-14

US-09-761-636A-14

US-09-761-636A-14

US-09-761-636A-16

US-10-253-286-332

US-10-253-286-332

US-10-245-871-332

US-10-398-104-155

US-10-126-845-89

US-10-126-845-89

US-10-154-884B-11221
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                                                                                                                                                                                                                                                                                                                              1298764 seqs, 315065143 residues
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                                                                      OM protein - protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                              1 CISVPLTSVPC 11
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Perfect score:
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Sequence 11250, A Sequence 11254, A Sequence 11258, A Sequence 11255, A Sequence 11255, A Sequence 11275, A Sequence 11275, A Sequence 1011, Appl Sequence 10, Appl Sequence 12, Appl Sequence 11, Appl Sequence 24, Appl Appl Appl Appl Appl Appl Appl App	,
US-10-154-884B-11250 US-10-154-884B-11254 US-10-154-884B-11258 US-10-154-884B-11259 US-10-154-884B-11259 US-10-154-884B-11269 US-10-154-884B-11269 US-10-154-884B-11269 US-10-154-884B-11269 US-10-154-884B-11269 US-10-154-884B-11269 US-10-158-10-19 US-10-16-158-10-19 US-10-158-10-19 US-10-158-10-19 US-10-158-10-19 US-10-158-10-19	ALIGNMENTS
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RESULT 1
US-09-761-636A-7
Sequence 7, Application US/09761636A
Fatent No. US20020065218A1
GENERAL INFORMATION:
APPLICANT: ACHEN, Marc
APPLICANT: STACKER, Steven
APPLICANT: CENDRON, Angela
FILE REFERENCE: 1064/48505 Achen et al
TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
FILE REFERENCE: 1064/48505 Achen et al
FILE REPERENCE: 1064/48505 Achen et al
TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
FILE OF INVENTION NUMBER: US 60/176,293
PRIOR PPLICATION NUMBER: US 60/176,293
PRIOR PELING DATE: 2000-01-18
PRIOR FILING DATE: 2000-05-16
PRIOR FILING DATE: 2000-05-16
SOFTWARE: Patentin version 3.0
LENGTH: 11
FYEB: PRT
CORGANISM: Homo sapiens
US-09-761-636A-7

QUETY MATCH
BEST LOCAL Similarity 100.0%; Pred: No. 0.0036;
Matches 11; Conservative 0; Mismatches 0; Indels
Db I CISVPLTSVPC 11
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Db 1 CISVPLTSVPC 11
RESULT 2

0

US-09-761-636A-23 ; Sequence 23, Application US/09761636A ; Patent No. US20020065218A1 ò

SEQ ID NO 23

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| GENERAL INFORMATION:
| APPLICANT: ACHEN, Marc
| APPLICANT: ACHEN, Marc
| APPLICANT: BUGHES, Richard
| APPLICANT: CENDRON, Angela
| TITLE OF INVENTION: VGGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
| TITLE OF INVENTION NUMBER: US/09/761,636A
| CURRENT FILING DATE: 2000-01-18
| PRIOR PILING DATE: 2000-01-16
| NUMBER OF SEQ ID NOS: 34
| SOFURARE: PALENTIN VERSION 3.0
| SEQ ID NO 25
| LENGTH: 11
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Sequence 13, Application US/09761636A

Patent No. US20020065218A1

GENERAL INFORMATION:

APPLICANT: ACHEK, Marchard

APPLICANT: HUGHES, Richard

APPLICANT: CENDRON, Angela

TILLE OF INVENTION: VGGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR

FILE REFERENCE: 1064448505 Achen et al

CURRENT APPLICATION NUMBER: US/09/761,636A
TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85.2%; Score 52; DB 9; Length 11; 72.7%; Pred. No. 0.095; 1ive 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                          Length 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                          Score 54; DB 9;
Pred. No. 0.046;
                      FILE REFERENCE: 1064/48505 Achen et al CURRENT APPLICATION NUMBER: US/09/761,636A CURRENT FILING DATE: 2001-01-18
PRIOR PILING DATE: 2000-01-18
PRIOR FILING DATE: 2000-01-18
PRIOR FILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 34
NOFTWARE: Patentin version 3.0
SEQ ID NO 24
                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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Best Local Similarity 72.7%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                      synthetic construct
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Matches 8, Conservative
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1 CISLPISSVPC 11
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1 CITIPLTSLPC 11
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                                                                                                                                                                                                                                                                                               TYPE: PRT
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Sequence 26, Application US/09761636A

Patent No. US20020065218A1

GENERAL INFORMATION:

APPLICANT: APPLICANT: Steven

APPLICANT: CENUBRON, Angela

TITLE OF INVENTION: VEGF-D/VEGF PEPTIDOMIMETIC INHIBITOR

TITLE OF INVENTION: VEGF-D/VEGF PEPTIDOMIMETIC INHIBITOR

TITLE OF INVENTION: VEGF-D/VEGF PEPTIDOMIMETIC INHIBITOR

FILE REFERENCE: 1064/48805 Achen et al

CURRENT FILING DATE: 2001-01-18

PRIOR APPLICATION NUMBER: US 60/176,293

PRIOR FILING DATE: 2000-01-18

PRIOR FILING DATE: 2000-01-18

PRIOR FILING DATE: 2000-05-16

NUMBER OF SEQ ID NOS: 34

SEQ ID NOS: 34

SEQ ID NOS: 34

SEQ ID NO 26

TENGTH. 11
                              APPLICANT: ACHEN, Marc
APPLICANT: STACKER, Steven
APPLICANT: STACKER, Steven
APPLICANT: BAPLICANT: ACHEN
APPLICANT: BAPLICANT: CENDRON, Angela
TITLE OF INVENTION: VEGF-O/VEGF PEPTIDOMIMETIC INHIBITOR
FILE REFERENCE: 1064/48505 Achen et al
FILE REFERENCE: 1064/48505 Achen et al
CURRENT APPLICATION NUMBER: US/09/761,636A
CURRENT PILING DATE: 2001-01-18
PRIOR APPLICATION NUMBER: US 60/204,590
PRIOR PILING DATE: 2000-01-18
PRIOR APPLICATION NUMBER: US 60/204,590
PRIOR PILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PALENTIN VEYSION 3.0
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Pred. No. 0.0074;
1; Mismatches 0; Indels
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81.8%; Pred. No. 0.015;
tive 2; Mismatches (
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Patent No. US20020065218A1
GENERAL INFORMATION:
APPLICANT: ACHEN, MATC
APPLICANT: STACKER, Steven
APPLICANT: HUGHES, Richard
APPLICANT: CENDRON, Angela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: synthetic construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 96.7%;
Best Local Similarity 90.9%;
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 81.0.
Best Local 9; Conservative
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1 CLSVPLTSVPC 11
               GENERAL INFORMATION:
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LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
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; ORGANISM: Homo sapiens
US-10-253-286-332
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                                                                                                US-09-761-636A-10
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                   SEQ ID NO 10
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Sequence 14, Application US/09761636A

Patent No. US20020065218A1

GENERAL INCORMATION:

APPLICANT: APPLICANT: STACKER, Steven

APPLICANT: CENDRON, Angela

TITLE OF INVENTION: VEGF-D/VEGF-PEPTIDOMIMETIC INHIBITOR

FILE REFERENCE: 1064/48505 Achen et al

TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF-PEPTIDOMIMETIC INHIBITOR

FILE REFERENCE: 1064/48505 Achen et al

CURRENT APPLICATION NUMBER: US/09/761,636A

CURRENT PILING DATE: 2010-01-18

PRIOR FILING DATE: 2000-01-18

PRIOR FILING DATE: 2000-01-16

NUMBER: OF SOOTHWARE: US 60/204,590

PRIOR FILING DATE: 2000-05-16

NUMBER: OF SEQ ID NOS: 34

SOFTWARE: PATENTIN VERSION 3.0

SEQ ID NO 14

LENGTH: 9
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APPLICANT: STACKER, Steven
APPLICANT: STACKER, Steven
APPLICANT: STACKER, Steven
APPLICANT: CENDRO, Angela
TITLE OF INVENTION: VECF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
FILE REPERENCE: 1064/48505 Achen et al
CURRENT APPLICATION NUMBER: US/09/761,636A
CURRENT FILING DATE: 2000-01-18
PRIOR APPLICATION NUMBER: US 60/176,293
PRIOR PILING DATE: 2000-01-18
PRIOR APPLICATION NUMBER: US 60/204,590
PRIOR FILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2;
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Pred. No. 0.93;
0; Mismatches 0; Indels
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81.8%; Pred. No. 1.2e+06;
ive 0; Mismatches 0; Indels
PRIOR FILING DATE: 2000-01-18
PRIOR APPLICATION NUMBER: US 60/204,590
PRIOR FILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin version 3.0
SEQ ID NO 13
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 10, Application US/09761636A Patent No. US20020065218A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                   74.6%;
90.9%;
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Best Local Similarity 90.9
Matches 10; Conservative
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Best Local Similarity 81.8
Matches 9, Conservative
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                                                                                                                                                              ORGANISM: Homo sapiens
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; ORGANISM: Homo sapiens
US-09-761-636A-14
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US-09-761-636A-14
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Publication No. US20040058881A1
GENERAL INFORMATION:
APPLICANT: HUMPHREYS, ROBERT
APPLICANT: WIN MINZHEN
ITILE OF INVENTION: 11-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
FILE REFERENCE: REH-2015
CURRENT APPLICATION NUMBER: US/10/253,286
CURRENT PILING DATE: 2003-01-13
FRIOR APPLICATION NUMBER: 10/197,000
PRIOR FILING DATE: 2002-07-17
PRIOR FILING DATE: 2009-09-14
NUMBER OF SEQ ID NOS: 905
SSCHWARE: Patentin Ver. 2.1
SEQ ID NO 332
LENGTH: 9
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| Publication No. US20030235594A1
| GENERAL INFORMATION |
| APPLICANT: HOWPHERYS, ROBERT |
| APPLICANT: HOWPHERYS, ROBERT |
| TITLE OF INVENTION: IL-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES |
| FILE REFERENCE: REH-2013 |
| CURRENT APPLICATION NUMBER: US/10/245,871 |
| CURRENT APPLICATION NUMBER: 0/197,000 |
| PRIOR PILING DATE: 2003-07-17 |
| PRIOR FILING DATE: 2002-07-17 |
| PRIOR FILING DATE: 1999-09-14 |
| NUMBER OF SEQ ID NOS: 905 |
| SEQ ID NO 332 |
| LINGTH: 9
                                                              Gaps
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                                                           Indels
                   Length 9;
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DB 9; Lens.
1.1.2e+06;
0;
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47.5%; Score 29; DB 15;
Best Local Similarity 71.4%; Pred. No. 1.2e+06;
Matches 5; Conservative 1; Mismatches 1;
             52.5%; Score 32; DB 100.0%; Pred. No. 1.2 tive 0; Mismatches
        Query Match 52.5
Best Local Similarity 100.
Matches 7; Conservative
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Best Local Similarity 71.45
Matches 5; Conservative
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Gaps

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APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
TITLE OF INVENTION: Hematological Malignancies
TITLE OF INVENTION: Hematological Malignancies
TITLE OF INVENTION: WHERE: US/10/154,884B
CURRENT APPLICATION NUMBER: US 60/186,126
PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,779
PRIOR APPLICATION NUMBER: US 60/200,779
PRIOR APPLICATION NUMBER: US 60/200,999
PRIOR APPLICATION NUMBER: US 60/200,999
PRIOR APPLICATION NUMBER: US 60/200,999
PRIOR APPLICATION NUMBER: US 60/200,084
                                                                                                                                                                                                                                                                                                                                              JUNEARLY LAW CANDALOW:

JENDERALL LAW CANDALOW:

APPLICANT: Lambkin, Imelda J.

APPLICANT: Lambkin, Imelda J.

APPLICANT: Lambkin, Imelda J.

APPLICANT: Pinhila, Clemencia

APPLICANT: Propertor.

TITLE OF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM

TITLE OF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM

CURRENT APPLICATION NUMBER DE 1010/126,845

CURRENT FILING DATE: 2002-10-15

NUMBER OF SEQ ID NOS: 119

SEQ ID NO 89

LENGTH: 11
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45.5%; Pred. No. 4.2e+02;
Live 1; Mismatches 5; Indels
Score 29; DB 12; Length 11; Pred. No. 4.2e+02; 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: MISC FEATURE LOCATION: (1)...(11)
OTHER INFORMATION: D form retroinversion peptide
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Publication No. US20040005561A1
GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
                                                                                                                                                                                                                                                                           ; Sequence 89, Application US/10126845; Publication No. US20030181367A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: D form peptide
     Query Match

Best Local Similarity 36.4%;
Matches 4; Conservative ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
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Matches 5; Conservative
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US-10-154-884B-11221
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Pred. No. 4.2e+02;
3; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: LOS peptide mimotope sequence US-10-398-104-155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Mismatches
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APPLICANT: Letesson, Jean-Jacques
APPLICANT: Letesson, Jean-Jacques
APPLICANT: Letesson, Jean-Jacques
APPLICANT: Mertens, Pascal Yvon
APPLICANT: Woel, Pierre
APPLICANT: Woel, Pierre
FILE REFERENCE: B45242
CURRENT APPLICATION NUMBER: US/10/398,104
CURRENT APPLICATION NUMBER: PCT/EP01/11409
PRIOR FILING DATE: 2001-10-03
PRIOR FILING DATE: 2001-10-03
PRIOR FILING DATE: 2001-10-03
NUMBER OF SEQ ID NOS: 352
SOFTWARE: PastSEQ for Windows Version 4.0
SSOFTWARE: 11
                                                                                                                                                                           US-10-398-104-155
; Sequence 155, Application US/10398104
; Publication No. US20040047880A1
; GENERAL INFORMATION:
; APPLICANT: Letesson, Jean-Jacques
; APPLICANT: Lobet, Yves
; APPLICANT: Mertens, Pascal Yvon
; APPLICANT: Poolman, Jan
; APPLICANT: Poolman, Jan
; APPLICANT: Poolman, Jan
; APPLICANT: Poolman, Jan
; APPLICANT: Voet, Pierre
; TILE OF INVENTION: COMPONENT FOR VACCINE
; FILE REFERENCE: B45242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/398,104
CURRENT FILING DATE: 2003-01-04
PRIOR APPLICATION NUMBER: PCT/EP01/11409
PRIOR FLING DATE: 20001-10-03
PRIOR APPLICATION NUMBER: GB 0024200.8
PRIOR FILING DATE: 2000-10-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 352
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 155
LENGTH: 11
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Best Local Similarity 27.3*
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                                                 VPLTSVP 10
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US-10-398-104-156
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Search completed: September 5, 2004, 10:52:48 Job time : 67 secs
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PRIOR FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: US 60/206,201
PRIOR FILING DATE: 2000-05-22
PRIOR PILING DATE: 2000-05-14
PRIOR PILING DATE: 2000-07-14
PRIOR PILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-08-03
Remaining Frior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 11290
SOFTWARE: FastSEQ for Windows Version 3.0
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44.3%; Score 27; DB 15; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 11228, Application US/10154884B; Publication No. US20040005561A1; GENERAL INFORMATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 57.1
Best Local 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
CORGANISM: Homo sapiens
US-10-154-884B-11221
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US-10-154-884B-11228
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2 CLSVPVS 8
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US-10-154-884B-11228
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1 CISVPL 6
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4 CLSVPV 9
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RESULT 1
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                                                                                                              September 5, 2004, 10:45:30; Search time 20 Seconds (without alignments) 28.394 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /egn2_6/ptodata/2/jaa/5A_COMB.pep:*
/cgn2_6/ptodata/2/jaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/jaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/jaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/jaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/jaa/PCTUS_COMB.pep:*
           GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-438-150-1
US-08-340-28-154
US-09-601-729-204
US-08-836-075A-187
US-08-549-008-42
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US-08-170-068-150
US-08-900-321-5
US-08-900-321-5
US-08-189-331-149
US-08-189-331-149
US-08-331-333-149
US-08-331-333-149
US-08-331-333-149
US-08-331-333-149
US-08-331-333-149
US-08-800-3381-143
US-08-860-2381-143
US-08-860-2381-143
US-08-860-2381-143
US-08-861-108-26
US-08-861-108-26
US-08-861-108-26
US-08-861-228-108
US-08-861-228-108
US-08-861-238-108
US-08-861-28-108
US-08-861-28-108
US-08-861-38-108
US-08-861-38-108
US-08-861-38-108
US-08-861-38-108
US-08-861-38-108
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                                                                                                                                                                                                                                                                                                                    389414 seqs, 51625971 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                              OM protein - protein search, using sw model
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Match Length DB
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Maximum DB seq length: 11
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No.
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61, Appl
147, App
148, App
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19, Appl
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Patent No. 5747334
GENERAL INFORMATION:
APPLICANT: Kay, B. K.
APPLICANT: Fowlkes, D. M.
TITLE OF INVENTION: Totally Synthetic Affinity Reagents
NUMBER OF SEQUENCES: 186
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                        Score 30; DB 1; Length 8; Pred. No. 3e+05; 2; Indels
US-08-802-981-144
US-08-189-331-144
US-08-189-331-144
US-08-189-331-148
US-08-340-283-61
US-08-471-068-148
US-08-471-068-148
US-08-46-08-48
US-08-46-08-348-3
US-08-46-68-548-3
US-08-46-68-548-3
US-08-46-68-348-3
US-08-46-68-348-3
US-08-46-68-348-3
US-08-46-68-348-3
US-08-46-68-348-3
US-08-46-58-3
US-08-46-58-3
US-09-39-579-19
US-09-38-48-33-3
US-09-38-48-38-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICALL.
FILING DATE: CONCURRENTLY DELEWIC.
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MISTOCK, S. Leealie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-155
TELECOMUNICATION INFORMATION:
TELEFHONE: 212 790-9090
TELEFAK: 66141 PENNIE
FILER: 66141 PENNIE
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
"""" amino acids
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Best Local Similarity 62.5
Matches 5; Conservative
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44.3%;
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Best Local Similarity 62.5.
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                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 VPLTSVPC 11
                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 VPPAPVPC 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-212-190A-5
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US-08-900-321-5
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Sequence 5, Application US/08212190A
Septent No. 5652223
GENERAL INFORMATION:
APPLICANT: LIOTTA, Lance A
APPLICANT: KIN, Young Sook
TITLE OF INVENTION: DNA ENCODING CAI RESISTANCE PROTEINS AND
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOwnsend and Townsend and Crew
  Sequence 150, Application US/08471068
Patent No. 5948635
GENERAL INFORMATION:
APPLICANT: Kay, B. K.
APPLICANT: POWLKES, D. M.
TITLE OF INVENTION: Totally Synthetic Affinity Reagents
CORRESPONDENCES: 186
CORRESPONDENCES: 186
ADDRESSEE: Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49.2%; Score 30; DB 2; Length 8; ilarity 62.5%; Pred. No. 3e+05; Conservative 1; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                         OFFINANCE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTLING DATE:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-155
TELECOMMUNICATION INFORMATION:
TELERANCE: 212 790-9090
TELERAX: 212 869-8864/9741
TELEX: 66141 PENNIE
JINFORMATION FOR SEQ ID NO: 150:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                      E: Pennie & Edmonds
1155 Avenue of the Americas
                                                                                                                                                                                                   STREET: 1155 Avenue of the America CITY: New York STATE: New York CUMTRY: U.S.A. ZIP: 10036-2711 COMPUTER READBLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OMPATER: IBM PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/189,331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , MOLECULE TYPE: peptide US-08-471-068-150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unknown
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Best Local Similarity
Matches 5; Conserv
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US-08-471-068-150
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Gaps
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; Sequence 5, Application US/08900321
; Patent No. 5981712
; GENERAL INFORMATION:
; APPLICANT: Kohn, Elise C.;
; APPLICANT: Liotta, Lance A.;
; TITLE OF INVENTION: DAN Encoding CAI Resistance Proteins and
; TITLE OF INVENTION: Uses Thereof
; VUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Bighth Floor
; CITY: San Francisco
; CITY: California
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMFUTER: IBM PC compatible
COMFUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
CLASSIPTCATION NUMBER: US/08/212,190A
FILING DATE: 14-MAR-1994
CLASSIPTCATION: 435
FILING DATE: 14-MAR-1994
FREISTRATION NUMBER: 38,498
REGISTRATION NUMBER: DHHS Ref. No. 5652223 E-112-94/0
FILEPHONE: (415) 543-5600
FILEPHONE: (415) 543-5600
FILEPHONE: (415) 543-5603
FILEPHONE: CHARACTERISTICS:
LEWGTH: 10 amino acide
FIREPHONE: Amino acide
FIREPHONE: Amino acide
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Pred. No. 1.6e+02;
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REFERENCE/DOCKET NUMBER: 015280-204100US
TELECOMMUNICATION INPORMATION:
TELEPHONE: (415) 576-0200
TELEPAS: (415) 576-0300
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/212,190
FILING DATE: 14-MAR-1994
ATTORNEY/AGENT INFORMATION:
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FILE REFERENCE: BRU96-02
                                                                                                                              ; TYPE: PRT
; ORGANISM: Rat
US-08-769-745-15
                                                                                                                                                                                                                                                                                                                                                                                      US-08-189-331-149
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US-08-471-068-149
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                                                                                                                                           Score 27; DB 2; Length 10;
Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 27; DB 5; Length 10;
Pred. No. 1.6e+02;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 6
US-08-769-745-15
Sequence 15, Application US/08769745
Facture No. 5955259
GENERAL INFORMATION:
APPLICANT: Holmes, Todd C.
APPLICANT: Levitan, Irwin B.
APPLICANT: Brandeis University
TITLE OF INVENTION: Mechanism for the Regulation of Ion
TITLE OF INVENTION: Channel Activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 15280-204000PC
REFERENCE/DOCKET NUMBER: DHHS Ref. No. E-112-94/0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: PATENTIN DATA:
APPLICATION NUMBER: PCT/US95/03610
FILING DATE: 14-MAR-1995
CLASSIFICATION:
                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/212,190
FLIING DATE: 14-WAR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                    Sequence 5, Application PC/TUS9503610 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
TITLE OF INVENTION: DNA ENCODING
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 10
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                         44.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44.3%;
              LENGTH: 10 amino acids TYPE: amino acid STRANDEDNESS:
                                                                                                                     Query Match
Best Local Similarity 62.5
The Si Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 10 amino acids
amino acid
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Conservative
                                                                 ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-900-321-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide
                                                                                                                                                                                                             4 VPLTSVPC 11
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                                                                                                                                                                                                                                                1 VPPAPVPC 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                RESULT 5
PCT-US95-03610-5
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Kay, B. K.
APPLICANT: Fowlkes, D. M.
TITLE OF INVENTION: Totally Synthetic Affinity Reagents
                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                 42.6%; Score 26; DB 2; Length 6; 83.3%; Pred. No. 3e+05; 1ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42.6%; Score 26; DB 1; Length 8; 57.1%; Pred. No. 3e+05; 2; Indels live 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U.S.A.

ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/189,331
FILING BATE: CONCURENTLY herewith
CLASSIFICATION: 435
CURRENT APPLICATION NUMBER: US/08/769,745
CURRENT FILING DATE: 1996-12-19
NUMBER OF SEQ ID NOS: 41
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18,872
FR: 1101-155
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 149, Application US/08189331
Patent No. 5747334
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFRENCE/COCKET NUMBER: 1101
TELECOMMUNICATION INFORMATION:
TELEFAX: 212 790-909
TELESAX: 212 869-864/9741
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 8 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: TO NUMBER OF SEQUENCES: 1 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide
                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                   5 PLTSVP 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                             PLTPVP 6
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TOPOLOGY: linear MOLECULE TYPE: peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                               2 AIPM-SIPC 9
                                                                                                                                                                                                                                                               STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 10
US-08-549-008-43
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              Patent No. 5948635
GENERAL INPORMATION:
APPLICANT: Ray, B. K.
APPLICANT: Fowlkes, D. M.
TITLE OF INVENTION: Totally Synthetic Affinity Reagents
TITLE OF INVENTION: Totally Synthetic Affinity Reagents
TUMBER OF SEQUENCES: 186
CORRESPONDENCE ADDRESS:
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 8;
                                                                                                                                                                       STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 26; DB 2;
Pred. No. 3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
Sequence 149, Application US/08471068
                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/189,331
                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Misrock, S. Leslie

RECISTRATION NUMBER: 18,872

REFERENCE/DOCKET NUMBER: 1101-

TELECOMMUNICATION:

TELEPHONE: 212 790-9090

TELEX: 66141 PENNIE

INPORMATION FOR SEC ID NO: 149:

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 8 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 CVSAPQT 8
                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-471-068-149
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CURRENT APPLICATION NATAL AND ATTIONS APPLICATION WHORER 19, 98 / 98 / 931, 383

PLILOR DATE: 28 - 907-1394

ATTIONS AND ATTIONS 444

ATTIONS AND ATTIONS 454

REPRESENCE/COCKET NUMBER: 29, 664

REPRESENCE/COCKET NUMBER: 20, 762

REPRESENCE/COCKET NUMBER: 20, 76
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Gaps
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Patent No. 5811391

GENERAL INFORMATION:
APPLICANT: Arrhenius, Thomas S.
APPLICANT: Tempczyk, Anna
APPLICANT: Compcsition S.
TITLE OF INVENTION: Cyclic CS-1 Peptidomimetics,
TITLE OF INVENTION: Compositions and Methods of Using Same
NUMBER OF SEQUENCES: 33
CORRESPONDENCE: 33
CORRESPONDENCE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    spectral MS/MS techniques
RMATION: Phakellistatin 10 is a
RMATION: cell growth inhibitory peptide with
RMATION: activity in murine lymphocytic leukemia
RMATION: cell line of 2.1 mg/ml.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41.0%; Score 25; DB 1; Length 8; 66.7%; Pred. No. 3e+05; 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: amino acid analysis, high resolution NAME/KEY: nuclear magnetic resonance and mass
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3: Campbell & Flores LLP
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                    ZIP: 85258-1234
COMPUTER READABLE FORM:
MEDIUM TYPE: Distette, 3.5 inch, 1.44 Mb
                                                                                                                                                                                                                                    COMPUTER: IBM ES/2
COMPUTER: IBM ES/2
SOFTWARE: Microsoft Word for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/360,239B
FILING DATE: 12/20/94
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Richard R. Mybeck
REGISTRATION NUMBER: 17,886
REFRENCE/DOCKET NUMBER: 4997
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Richard R. Mybeck
STREET: 8010 East Morgan Trail, #10
CITY: Scottsdale
                                                                                                                                                                                                                                                                                             Word for Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORIGINAL SOURCE:
ORGANISM: Phakellia sp.
DEVELOPMENTAL STAGE: whole organism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
DESCRIPTION: Cyclooctapeptide
DESCRIPTION: phakellistatin 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 8 amino acid residues TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: Phakellistatin 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (602)-483-128
TELEFAX: (602)-483-7452
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 66.73,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      circular
                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
US-08-360-239B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cyclic
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                                                                                                                                   Arizona
: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 PLTSVP 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-483-077C-26
                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 13
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                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Komoriya, Akira
APPLICANT: Reverly S.
TITLE OF INVENTION: Compositions for the Detection of Enzyme
TITLE OF INVENTION: Activity in Biological Samples and Methods of Use Thereof
NUMBER OF SEQUENCES: 231
CORRESPONDENCE ADDRESS:
                                                                                                                              1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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                                                                                                                           Gaps
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Fatent No. 5801222
Fatent No. 5801222
FATENT NO. 5801222
FAPLICANT: Pettit, George R.
FAPLICANT: Tan, Rui
TITLE OF INVENTION: Isolation and Structure of
TITLE OF INVENTION: the Human Cancer Cell Growth Inhibitory Cyclic
TITLE OF INVENTION: Octapeptides Phakellistatin 10 and 11
                                                                                                                           1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                  Query Match
41.8%; Score 25.5; DB 1; Length 9;
Best Local Similarity 44.4%; Pred. No. 3e+05;
Matches 4; Conservative 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 25.5; DB 3; Length 9;
Pred. No. 3e+05;
4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA

ZIF: 9411-3834

COMPUTER PAINL-3834

COMPUTER PEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAIDLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/802,981
FILING DATE: 20-FEB-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HULLE-T, TOM
REGISTRATION NUMBER: 38,496
REFERENCE/POCKET NUMBER: 38,496
REFERENCE/POCKET NUMBER: 016865-000300US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 143:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
"WAND: amino acids
"WAND: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                     ; Sequence 143, Application US/08802981
; Patent No. 6037137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Conservative
; MOLECULE TYPE: peptide US-08-549-008-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: San Francisco
STATE: California
                                                                                                                                                             3 SVPLTSVPC 11
                                                                                                                                                                                       ::|: |:||
2 AIPM-SIPC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 SVPLTSVPC 11
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AIPM-SIPC 9
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Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                        RESULT 11
US-08-802-981-143
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US-08-360-239B-1
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Gaps
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APPLICANT: Teng-Law, Janet

APPLICANT: KObori, Joan A.

APPLICANT: Al-Abdaly, Fahad A.

APPLICANT: Al-Abdaly, Fahad A.

APPLICANT: Guillermo, Roy

APPLICANT: Guillermo, Sam L.

APPLICANT: Deans, Kobert J.

TITLE OF INVENTION: POSITIVE AND POSITIVE/NEGATIVE CELL

TITLE OF INVENTION: SELECTION MEDIATED BY PEPTIDE RELEASE

NUMBER OF SEQUENCES: 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41.0%; Score 25; DB 2; Length 10; 66.7%; Pred. No. 3.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                           Score 25; DB 2; Length 10;
Pred. No. 3.4e+02;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                          LOCATION: 10
; LOCATION: 10
; OTHER INFORMATION: /note= "The carboxy-terminus is a
; OTHER INFORMATION: carboxamide."
15.08-519-109B-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: Usa

ZIP: 92713-5210

ZIP: 92713-5210

ZIP: 92713-5210

ZIP: 92713-5210

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,228

FILING DATE: 07-UN-1995

CLASSIFICATION 435

ATTORNEY/AGENT INFORMATION:
NAME: Guthrie, Janice
REGISTRATION NUMBER: 17-4630CIP3

REFERENCE/DOCKET NUMBER: 17-4630CIP3

TELECOMMUNICATION INFORMATION:
TELEPHONE: (714) 553-1952

INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
LENGTH: Line anime acids

LENGTH: Line anime acids
REFERENCE/DOCKET NUMBER: P-CY 1795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Janice Guthrie, Ph.D.
STREET: P.O. Box 15210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 108, Application US/08482228 Patent No. 5968753
                     TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPACK: (619) 535-9849
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 44.4%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide US-08-482-228-108
                                                                                                                                                                                                                                MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 ISVPLTSVP 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 LDVPILDVP 10
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                                                                                                                                                                                                                                                                                  NAME/KEY: Peptide
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Best Local Similarity
                                                                                                                                                                           TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Irvine
STATE: Califor
COUNTRY: USA
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Sequence 26, Application US/08519109B

Sequence 26, Application US/08519109B

Patent No. 586944B

GENERAL INFORMATION:
APPLICANT: Arrhenius, Thomas S.
APPLICANT: Elices, Mariano J.
APPLICANT: Zheng, Zhong-Li

TITLE OF INVENTION: Compositions and Methods of Using Same
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSER: Campbell & Plores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
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41.0%; Score 25; DB 2; Length 10;
Best Local Similarity 44.4%; Pred. No. 3.4e+02;
Matches 4; Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 10 OTHER INFORMATION: /note= "The carboxy-terminus is OTHER INFORMATION: carboxamide."
                                                                                                    CAPTURE TRADABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Plan Pr Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,077C
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: P-CY 1647
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 535-9901
TELEPRATIC (619) 535-9901
TELEPRATIC (619) 535-8949
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acide
TYPE: Amino acide
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/519,109B
FILING DATE: 25-AUG-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
                                          California
: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide
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               San Diego
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Matches 6; Conservative 0; Mismatches 3; Indels

o O

0; Gaps

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Search completed: September 5, 2004, 10:48:51 Job time: 21 secs

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RESULT 3
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                                                                                                  September 5, 2004, 10:52:56; Search time 21 Seconds (without alignments) 77.869 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                283366 seqs, 96191526 residues
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                                                               OM protein - protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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PH1472
PH1472
PH1480
S47394
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S26549
G44965
PH1463
PH1466
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PH1474
PT0217
S47381
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Match Length DB
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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seg length: 17
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Maximum DB &
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T-cell receptor be IG H chain V-D-J r T-cell receptor be T-cell antigen rec alpha-conotoxin GI T-cell antigen rec	.RS) - mouse (fragment) 10-Mar-1994 #text_change 11-Apr-1995 rr, H.; Barra, C.; Pannetier, C.; Regnault, A.; Ko nd recognition of two class I major histocompatib 21; PMID:8436911	DB 2; Length 16; 70; ches 3; Indels 0; Gaps 0;	4-1-G.4) - mouse (fragment) 31-Dec-1991 #text_change 30-May-1997 H.; Kishimoto, T. f islet beta cell-reactive T cells is not restric 21; PMID:1902501	s; DB 2; Length 12; 65; ches 1; Indels 1; Gaps 1;
PH1469 PH0931 PH0931 PH0753 PH0808 C49255 PH1467 PH	2R5)	Score 34; DB Pred. No. 70; 1; Mismatches	PESULT 2 PT016 T-cell receptor beta chain V-J region (4-1-G.4) C;Species: Mus musculus (house mouse) C;Decies: JD-cc-1991 #sequence_revision 31-Dec-1 C;Accession: PT0216 R;Nakano, N.; Kikutani, H.; Nishimoto, H.; Kish J. Exp. Med. 173, 1091-1097, 1991 A;Ttile: T cell receptor V gene usage of islet A;Reference number: PT0209; MUID:91217621; PMID A;Accession: PT0216 A;Accesion: PT0216 C;Keywords: T-cell receptor	Score 33.5; D Pred. No. 65; 1; Mismatches
HDDDDDDDDDDDDDD	lone e mc rej 933 ctic JiD.	* *	rev rev rev shi	
12 12 12 13 14 15 15 16 17 17 17 18 18 18 18 18 18 18 18 18 18 18 18 18	r beta chain (clone A3/H musculus (house mouse) 11994 #sequence_revision 11477 1177 1181-820, 1993 1 receptor selection by ber: PH1430; MUID:93171 11 mRNA 6 < CAS> source: cytolytic T-lym immunoglobulin homology immunoglobulin homology	34.0%; Larity 60.0%; Conservative ELGKSTN 10 : SVGTGTN 10	ca chain V-J ullus (house [# sequence_r	larity 72.7%; Conservative ELGKSTNT 11
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0 4 0000000000000000000000000000000000	ceptor beta c Mus musculu Muar-1994 #s on: PH1477 a, J.L.; Mart ed. 177, 811- T cell recept ce number: PH on: PH1477 e type: mRNA e type: mRNA fill source: fill so	1 8 8 1 1	receptor be eas: Mus mus 31-Dec-199 sion: PT021 Med. 173, T Kiku Med. 173, T T T T T T T T T T T T T T T T T T T	Match Local Similarity Les 8; Conserv 1 CASELGKSTN
и м и м и м и м и м и м и м и м и м и м	RESULT 1 PH1477 T-cell receptor C,Species: Nusr C,Accession: PH: K,Casnova, J.L. J. Exp. Med. 17. A,Title: T cell A,Accession: PH: A,Molecule type: A,Residues: 1-16 A,Experimentation: C,Superimentation: C,Superfamily: i	Query Matci Best Local Matches Qy	RESULT 2 PT0216 T-cell receptor beta C;Species: Mus muscul C;Date: 31-Dec-1991 # C;Accession: PT0216 R;NARANO, N.; Kikutan J. Exp. Med. 173, 109 A;Title: T cell recep A;Reference number: P A;Accession: PT0216 A;Molecule type: mRNA A;Residues: 1-12 .NAK C;Keywords: T-cell rec	Query Ma Best Loc Matches

1 CASSLG-TINT 10

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T-cell antigen receptor VJ junction beta chain - human C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C;Accession: S47364; S47369
R;Chener, P. J.
R;Dehner, P. J.
R;Description: Human HiA-A0201 restricted recognition of influenza A is dominated by T c A;Reference number: S47355
A;Accession: S47394
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Molecule type: mrnå
A,Residues: 1-12 <LEH>
A,Cross-references: BMBL:235714; NID:g527523; PIDN:CAA84783.1; PID:g527524; EMBL:235694;
C,Keywords: T-cell receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rilehner, P.J.

Rilehner, P.J.

Submitted to the EMBL Data Library, August 1994

A; Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T C

A; Reference number: 847355

A; Accession: §47357
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C;Species: Mus musculus (house mouse)
C;Decises: Mus musculus (house mouse)
C;Accession: 826549; 82656
B;Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Win Med. 176, 439-447, 1995
A;Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor A;Reference number: 826512; MUD: 92364546; PMID:1380061
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C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C;Accession: S47357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:Z35681; NID:g527451; PIDN:CAA84750.1; PID:g527452 C;Keywords: T-cell receptor
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Pred. No. 2.3e+02;
Pred. Tresher 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
     Indels
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        4.
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Pred, No. 2.9e+02;
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Best Local Similarity 63.6%;
Matches 7; Conservative
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A;Residues: 1-12 <CAS>
A;Cross-references: EMBL:X67999
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Best Local Similarity 50.0°
Matches 6; Conservative
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          Conservative
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                                                            1 CASELGKSTN 10
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A; Molecule type: mRNA
A; Residues: 1-13 < LEH>
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             Matches
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 11-Apr-1995
C;Accession: PH473
C;Accession: PH473
J; Martinon, F; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; KG
J; Exp. Med. 177, 811-820, 1993
A;Title: T cell receptor selection by and recognition of two class I major histocompatib
A;Reference number: PH1430; MUID:93171821; PMID:8436911
A;Accession: PH473
A;Molecule type: mRNA
A;Residues: 1-16 cAS>
A;Experimental source: cytolytic T-lymphocyte
C;Superfamily: immunoglobulin homology
C;Keywords: receptor; T-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Richards No. 11. Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; Kd. J. Exp. Med. 17., 811-820, 1993
A,Title: T cell receptor selection by and recognition of two class I major histocompatiby A,Reference number: PH1430; MUID:93171821; PMID:8436911
A,Accession: MH480
A,Molecule type: mRNA
A,Residues: 1-16 <CAS1>
     T-cell receptor beta chain (clone A24/12.2) - mouse (fragment)
C;Speciee: Mus musculus (house mouse)
C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 11-Apr-1995
C;Accession: PH1472
C;Accession: PH1472
J. Exp. Med. 177, 811-820, 1993
A;Title: T cell receptor selection by and recognition of two class I major histocompatib
A;Reference number: PH1430; MUID:93171821; PMID:8436911
A;Reference number: PH1430; MUID:93171821; PMID:8436911
A;Residues: 1-16 ccAS>
A;Molecule type: mRNA
A;Residues: 1-16 ccAS>
A;Reperimental source: cytolytic T-lymphocyte
C;Superfamily: immunoglobulin homology
C;Keywords: receptor; T-cell
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C;Species: Whus muscutlus (house mouse)
C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 27-Oct-1995
C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 27-Oct-1995
C;Accession: PH1480; PH1478
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                                                                                                                                                                                                                                                                                                                                                                                                        Score 32; DB 2; Length 16;
Pred. No. 1.4e+02;
0; Mismatches 4; Indels
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A;Molecule type: mRNA
A;Residues: 1-16 <CAS.2
A;Experimental source: cytolytic T-lymphocyte, clone A24/PEF5
C;Superfamily: immunoglobulin homology
C;Keywords: receptor; T-cell
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60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 60.0%;
Matches 6; Conservative
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Best Local Similarity
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Best Local Similarity
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R; Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; Ko J. Exp. Med. 177, 811-820, 1993
A; Fitle: T cell receptor selection by and recognition of two class I major histocompatib A; Reference number: PH1430; MUID:93171821; PMID:8436911
A; Accession: PH1463
A; Molecule type: mRNA
A; Residues: 1-12 cAs.
A; Experimental source: cytolytic T-lymphocyte
C; Superfamily: immunoglobulin homology
C; Keywords: receptor; T-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T-cell receptor beta chain (clone A3/74.1) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 11-Apr-1995
C;Accession: PH1466
R;Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; Ko A;Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; Ko A;Title: T cell receptor selection by and recognition of two class I major histocompatib A;Reference number: PH1430; MUID:93171821; PMID:8436911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C;Accession: S47400
R;Lehner, P.J.
R;Lehner, P.J.
A;Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T c A;Reference number: S47355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary
A;Nolcoule type: mRNA
A;Residues: 1-13 <LEM-3 <LEM-5
A;Cross-references: EMBL:Z35678; NID:g527535; PIDN:CAA84747.1; PID:g527536
C;Keywords: T-cell receptor
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Pred. No. 4.7e+02;
1; Mismatches 1; Indels
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28.0%; Score 28; DB 2; I
Local Similarity 62.5%; Pred. No. 4.7e+02;
les 5; Conservative 1; Mismatches 2.
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Pred. No. 5e+02;
2; Mismatches
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A; Residues: 1-12 < CAS>
A; Experimental source: cytolytic T-lymphocyte
C; Keywords: receptor; T-cell
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71.4%;
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41.7%;
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Best Local Similarity 71.4.
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Matches 5, Conservative
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C;Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 18-Jun-1993
C;Accession: 644457
R;Takeda, S.; Sato, F.; Ida, K.; Yamada, Y.
R;Takeda, S.; Sato, F.; Ida, K.; Yamada, Y.
A;Title: Characterization of polypeptides that accumulate in cultured Nicotiana tabacum A;Reference number: A44957
A;Accession: 644957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C)Accession: C24166
R;Vater, J.; Salnikow, J.; Jansson, C.
FEBS Lett. 203, 230-234, 1986
A;Title: N-terminal sequence determination and secondary structure analysis of extrinsic
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C,Date: 05-Jun-1987 #sequence_revision 21-May-1988 #text_change 24-Apr-1998
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C;Species: Mus musculus (house mouse)
C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 11-Apr-1995
C;Accession: PH.463
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                                                                  A.Residues: 1-12 <CA2>
A.Cross-references: EMBL:X68000
A.Cross-references: EMBL:X68000
A.Experimental source: cytolytic T-lymphocyte, clone Cw3/Cas1
C.Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: T-cell receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Superfamily: photosystem II oxygen-evolving complex protein 2 C;Keywords: chloroplast; membrane protein; thylakoid
                                                                                                                                                                                                                                Length 12;
                                                                                                                                                                                                                      Score 29; DB 2; Length 12;
Pred. No. 3.3e+02;
2; Mismatches 1; Indels
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Pred. No. 3.7e+02;
2; Mismatches 3; Indels
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Pred. No. 4.4e+02;
2; Mismatches 3; Indels
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A; Experimental source: cytolytic T-lymphocyte, clone Cw3/A9
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Best Local Similarity 50.0
Matches 5; Conservative
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                                                                                                                                                                                          CASSLGET 8
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A;Molecule type: protein
A;Residues: 1-14 <TAK>
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                                                Molecule type: mRNA; Residues: 1-12 <CA2>
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Query Match

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RESULT 11

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T-ucal, receptor beta chain V-J region (4-1-E.2) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 30-May-1997
C;Accession: PT0217
R;Nakano, N.; Kikutani, H.; Nishimoto, H.; Kishimoto, T.
T. Exp. Med. 173. 1091-1097, 1991
A;Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not restrict A;Reference number: PT0209; MuID:91217621; PMID:1902501
A;Reference number: mRNA
A;Residues: I-11 <NAK>
C;Keywords: T-cell receptor
PH1474
T-cell receptor beta chain (clone A2/25) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 11-Apr-1995
C;Accession: PH1474
S;Casanova, J.L.; Marthnon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; Kc
J. Exp. Med. 177, 811-820, 1993
A;Title: T cell receptor selection by and recognition of two class I major histocompatib
A;Reference number: PH1430, MUID:93171821; PMID:8436911
A;Reference number: PH1430, MUID:93171821; PMID:8436911
A;Residues: 1-16 <CAS-
A;Residues: 1-16 <CAS-
C;Superfamily: immunoglobulin homology
C;Keywords: receptor; T-cell
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Pred. No. 6.2e+02;
0; Mismatches 1; Indels
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28.0%; Score 28; DB 2; Length 16;
Best Local Similarity 50.0%; Pred. No. 6e+02;
Matches 5; Conservative 0; Mismatches 5; Indels
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Best Local Similarity 83.3
Matches 5; Conservative
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Search completed: September 5, 2004, 10:56:30 Job time: 21 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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PSP3 PHYPA
UC19 MAIZE
CXA1 CONGE
CXA2 CONGE
CXA4 CONST
PSBP PINPS
CXA1 CONCN
CXA1 CONAL
CXA2 CONBE
CXA2 CONBE
CXA3 CONBE
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CXST_CONTE
SODM STRGE
UR2B_CATCO
UR2B_CATCO
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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P04561 P83507 P83504 P83504 P21225 P2228 P23287 P23436 P11917 P10521 P107493	thogastropoda; '; Hypsogastropoda; Zhong MN.; Zhong MN.; OF CONOTOXINS. 1 CRC64; 1 LRC64; 22; Length 14; 22; 5; Indels 0;	Da subunit of nyta; Bryophyt Physcomitrell
UR2B_CYPCA UMP_CAVPO COM_CONVE C1QA_RAT C1QA_RAT CHII_PEA ONCI_ONCMY AHI_PRUSE GERB_RAT KTRC_AREMA BOLI_MEGPE BOL2_MEGPE BOL2_MEGPE	update) update) update) n update) poda; Ort eoconcha nus. KH., Z linus."; linus."; the venc THOD=MAILY ERFAMILY 3. 193432EB1 7; DB 1;	12 AA. 12 Date) ion update) (on update) (organent) (Fragment) hyta; Embryo
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112 112 113 114 114 117 117	STANDARD; 1. 41, Creal 1. 41, Last a. (Beech con Cacac) Mollus Cacac) Mollus Cacac) Mollus Cacac) SPECTRC Gonoidea; C 4; ASS SPECTRC 6; PubMed=1 CX., Hu DOCATION: IFTCITY: EX DMETRY: MW= BELONGS TO in. 9 12 13 A; 1597 MW SETVATIVE 13 A; 1597 MW SETVATIVE 13 A; 1597 MW SETVATIVE CACAC	STANDARD; 1. 34, Cr 1. 34, La 1. 40, La enhancer of photo patens (M diplantae riidae; F
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W W W W W W 4 4 4 4 4 4 4 4 4 4 4 4 4 4	RESULT 1 CXIA_CONI AC 28-15 DT 28-15 CON Neogon Neog	RESULT PSP3 PH ID PS AC P8 DT 01 DT 01 DT 02 DD 0C PN OC BT OX NC

SEQUENCE. TISSUE=Protonema; MEDLINE=97275459; PubMed=9129336;

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P80431 P58848 P58849

Conoidea; Conidae; Conus

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Neogastropoda; Co
NCBI_TaxID=6491;
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Pernollet J.-C., Zivy M., de Vienne D.;
"The maize two dimensional gel protein database: towards an integrated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                              Gaps
                                     -1- FUNCTION: May be involved in the regulation of photosystem II.
                                                                                                                                                                                                                                                                                                                                                                                                                                    genome analysis program.";
Theor. Appl. Genet. 93:997-1005(1996).
-!- MISCELLANBOUS: On the 2D-gel the determined pl of this unknown
protein is: 5.6, its MM is: 18.4 kDa.
Maize-2DPAGE; P80625; COLEOPTILE.
                                                                                                                                                                                                                                                                                                                                  Tracheophyta;
  Kasten B., Buck F., Nuske J., Reski R.; "Cytokinin affects nuclear- and plastome-encoded energy-converting
                                                            with the photosystem II complex.
-!- INDUCTION: By light.
-!- SIMILARITY: Belongs to the pabP family.
Photosynthesis; Photosystem II; Chloroplast; Thylakoid; Membrane;
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                                                                                                                                                                                                                                                                      01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Unknown protein from 2D-page of etiolated coleoptile (Spot 406)
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Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
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0
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
PACCAD clade, Panicoideae, Andropogoneae, Zea.
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21-JUL-1986 (Rel. 01, Last sequence update)
10-OTT-2003 (Rel. 42, Last annotation update)
Alpha-conotoxin GIA [Contains: Alpha-conotoxin GI (GI)].
Conus geographus (Geography cone).
                                                                                                                                        Score 26; DB 1; Length 12; Pred. No. 2.3e+02;
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12 AA; 1182 MW; 8D2B0D54D7C44DC5 CRC64;
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50.0%;
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                       plastid enzymes.";
Planta 201:261-272(1997).
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Best Local Similarity
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TISSUE=Coleoptile;
                                                                                                      Multigene family.
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GI determined by 1H nuclear distance geometry calculations.";
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BELLINE-25349531; Pubmed-7623764;

Groebe D.R., Dumm J.M., Levitan E.S., Abramson S.N.;

"alpha-Conotoxins selectively inhibit one of the two acetylcholine"
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Kobayashi Y., Ohkubo T., Kyogoku Y., Nishiuchi Y., Sakakibara S.,
Braun W., Go N.;
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Guddat L.W., Martin J.A., Shan L., Edmundson A.B., Gray W.R.;
"Three-dimensional structure of the alpha-conotoxin GI at 1.2-A
                                                                                                                                                                                                                                                                                                                                                                                                             DISJUBIDE BONDS OF GI, AND SYNTHESIS OF GI.
MEDLINE=84280842; PubMed=6466616;
Gray W.R., Luque F.A., Galyean R., Atherton E., Sheppard R.C.,
Stone B.L., Reyes A., Alford J., McIntosh M., Olivera B.M.,
Cruz L.J., Rivier J.;
"Conotoxin GI: disulfide bridges, synthesis, and preparation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MUTAGENESIS OF ARG-9.
MEDLINE=97317090; PubMed=9174364;
Groebe D.R., Gray W.R., Abramson S.N.;
Groebe D.R., Gray W.R., Abramson S.N.;
"Determinants involved in the affinity of alpha-conotoxins GI a
"Determinants involved in the affinity of alpha-cosptoxins GI.
For the muscle subtype of nicotinic acetylcholine receptors.";
Biochemistry 36:6469-6474 (1997).
                                                                                                                                                                                                                                                                            conotoxin GI, a neurotoxic
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Biochemistry 28:5494-5501(1989).
                         Gray W.R., Luque F.A., Olivera B.M., Barrett J., Cruz L.J.;
"Peptide toxins from Conus geographus venom.";
J. Biol. Chem. 256:4734-4740(1981).
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Maslennikov I.V., Sobol A.G., Gladky K.V., Lugovskoy A.A.,
Ostrovsky A.G., Tsetlin V.I., Ivanov V.T., Arsenlev A.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPARISON WITH ALPHA-CONOTOXIN SI AND ALPHA-CONOTOXIN MI
MEDLINE-95034849; PubMed=7947815;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      binding sites of nicotinic receptors.";
Mol. Pharmacol. 48:105-111(1995).
                                                                                                                                                                         DISULFIDE BONDS OF GI, AND SYNTHESIS OF
                                                                                                                                                                                                                                                                                                                 tridecapeptide from a marine snail.";
FEBS Lett. 148:260-262(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Solution conformation of conotoxin
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                                                                                                                                                                                                          MEDLINE=83105694; PubMed=7152021;
Nishiuchi Y., Sakakibara S.;
"Primary and secondary structure of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [9]
STRUCTURE BY NMR OF GI.
MEDLINE=89375269; PubMed=2775719;
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MEDLINE=81191854; PubMed=7014556;
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Biochemistry 23:2796-2802(1984).
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Biochemistry 38:11895-11904(1999).

Biochemistry Alpha-conotoxins act on postsynaptic membranes, they bind to the nicotinic acetylcholine receptors (nAChR) and thus inhibit them. The higher affinity site for alpha-conotoxin GI is the alpha/delta site on mouse muscle-deriverd BG3H-1 receptor, and the other site (alpha/damma site) on nicotinic receptors from
                                                                                                                                                                                                                                                                                                                                               Mok K.H., Han K.H.; "NMR solution conformation of an antitoxic analogue of alpha-conotoxin GI: identification of a common nicotinic acetylcholine receptor alpha(1)-subunit binding surface for small ligands and alpha-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AMIDATION (IN ALPHA-CONOTOXIN GIA).
R->A. REDUCTION (IN ALPHA-CONOTOXIN GIA).
R->A. REDUCTION IN AFFINITY FOR BOTH
ALPHA/DELTA AND ALPHA/GAWWA SITES ON
BC3H-1 RECEPTORS AND LOSS OF AFFINITY FOR
BOTH ALPHA/DELTA AND ALPHA/GAWWA SITES ON
TORPEDO RECEPTORS (IN GI).
"Two distinct structures of alpha-conotoxin GI in aqueous solution.";
Eur. J. Biochem. 254:238-247(1998)
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--- SUBCELLULAR LOCATION: Secreted.
--- TISSUE SPECIFICITY: Expressed by the venom duct.
--- SIMILARITY: Belongs to the conotoxin A-superfamily. Alpha-type
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bonds in
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                                                                         STRUCTURE BY NMR OF GI.

MEDLINE=98239743; PubMed=9571060;
Gehrmann J., Alewood P.F., Craik D.J.;
"Structure determination of the three disulfide bond isomers alpha-conocoxin GI: a model for the role of disulfide bonds structural stability.";
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Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
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Pred. No. 6.2e+02;
0; Mismatches 2; Indels
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ALPHA-CONOTOXIN GIA.
ALPHA-CONOTOXIN GI.
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MEDLINE=99438341; PubMed=10508392;
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1XGB; 16-FEB-99.
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                                                                                                                                                                                                                                                                                            STRUCTURE BY NMR OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             family.
A01782; NTKNAG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
nes 3; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1XGC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1083;
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MUTAGEN
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AC 201250;
DT 21-JUL-
DT 21-JUL-
DT 28-FEB-
DE Alpha-c
DE Alpha-c
OC Bukaryc
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Matches
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REAL STANTANT STANTAN
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Gaps
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-I. FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they bind to the nicotinic acetylcholine receptors (nAChR) and thus inhibit them.
                                                                                                                                                                                                                                                                                                                         -!- SUBCELLUIAR LOCATION: Secreted.
-!- TISSUB SPECIFICITY: Expressed by the venom duct.
-!- SIMILARITY: Belongs to the conotoxin A-superfamily. Alpha-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Alpha-conotoxins, small peptide probes of nicotinic acetylcholine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SUBCELLUAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Expressed by the venom duct.
-!- SIMILARITY: Belongs to the conotoxin A-superfamily. Alpha-type
   Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
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Conus striatus (Striated cone).

Ebkaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
Apogastropoda; Caenogastropoda; Gorbeoconcha; Hypsogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     receptors.";
Biochmistry 30:9370-9377(1991).
-!- FUNCTION: Alpha-conotoxins act on postsynaptic membranes,
bind to the nicotinic acetylcholine receptors (nAChR) and
inhibit them.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Myers R.A., Zafarella G.C., Gray W.R., Abbot J., Cruz L.J.,
Olivera B.M.;
                                                                                                  Cruz L.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23.0%; Score 23; DB 1; Length 13; 60.0%; Pred. No. 7.9e+02; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEEE831C39297EBD CRC64;
                                                                                                 Barrett J.,
                                                          SEQUENCE.
MEDLINE=81191854; PubMed=7014556;
Gray W.R., Luque A., Olivera B.M., Barrett J.,
"Peptide toxins from Conus geographus venom.";
J. Biol. Chem. 256:4734-4740(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                          family.

PIR; A01783; NTKN2G.

HSSP; P56973; 1B45.

Postsynaptic neurotoxin; Neurotoxin; Toxin; Accetylcholine receptor inhibitor; Amidation. DISULRID.
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MEDLINE=91369955; PubMed=1892838;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                              NCBI_TaxID=6491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13 CKPPC 17
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                                                                                                                                                         DISULFIDE BONDS
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P28878;
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MEDLINE=99255390; PubMed=10320362;
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                                                                                                                                         consors.";
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Matches
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Electrophoresis 20:1098-1108(1999).
Electrophoresis 20:1098-1108 in the regulation of photosystem II.
-!- FUNCTION: May be involved in the regulation of photosystem II.
-!- SUBGELIGIAR LOCATION: Chloroplast thylakoid membrane; associated with the photosystem II complex (By similarity).
-!- MISCELIANBOUS: On the 2D-gel the determined pI of this protein (spot NIT9) is: 5.9, its MW is: 22 kba.
-!- SIMILARITY: Belongs to the psbP family.
Photosynthesis; Photosystem II; Chloroplast; Thylakoid; Membrane.
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                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                        15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
0xygan-evolving enhancer protein 2 (OBE2) (23 kDa subunit of oxygen evolving system of photosystem II) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=99274088; PubMed=10344291;
Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
Frigerio J.-M., Plomion C.;
"Separation and characterization of needle and xylem maritime pine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Coniferopsida, Coniferales, Pinaceae, Pinus.
NCBI_TaxID=71647;
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Eppogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 13;
                                                                                                                                     Score 23; DB 1; Length 13;
Pred. No. 7.9e+02;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Indels
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16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last amotation update)
Alpha-conotoxin CnIA [Contains: Alpha-conotoxin CnIB].
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                                                                                   AMIDATION.
DEF1931982457EBD CRC64;
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40.0%; Pred. No. 7.9e+02;
tive 2; Mismatches 4;
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      Postsynaptic neurotoxin; Neurotoxin; Toxin; Acetylcholine receptor inhibitor; Amidation
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                                                                                                                                               23.0%;
60.0%;
                                                                                                          1461 MW;
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                                                                                                                                                                                         3; Conservative
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Best Local Similarity
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                                                                                                                                                              Local Similarity
                                                                                       13
3 AA;
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SEQUENCE
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SEQUENCE
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ID _PSBP_P
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Gaps
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                                                                                                 of Conus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -:- SUBCELLULAR LOCATION: Secreted.
-:- TISSUE SPECIFICITY: Expressed by the venom duct.
-:- SIMILARITY: Belongs to the conotoxin A-superfamily. Alpha-type
                                                                                                                                                        Biochemistry 38:6317-6326(1999).
-!- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they bind to the nicotinic acetylcholine receptors (nAChR) and thus inhibit them. This peptide seems to be a potent and selective
                                                                                                                                                                                                                                             blocker of muscular subtype of nAChR.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Expressed by the venom duct.
-!- SIMILARITY: Belongs to the conotoxin A-superfamily. Alpha-type
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Conus magus (Magus cone).

Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;

Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;

Neogastropoda; Conoidea; Conidae; Conus.
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                                                                             "Biochemical characterization and nuclear magnetic resonance
structure of novel alpha-conotoxins isolated from the venom (
  Lamthanh
                                                                                                                                                                                                                                                                                                                                                    family.
PIR, A58963,
PDB, 1845, 09-JUL.99.
Posteynaptic neurotoxin; Neurotoxin; Anidation; 3D-structure.
Acetylcholine receptor inhibitor; Anidation; 3D-structure.
Acetylcholine receptor inhibitor. Anidation; Alpha-CONOTOXIN CNIA.

ALPHA-CONOTOXIN CNIB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Indels
Favreau P., Krimm I., le Gall F., Bobenrieth M.J., La
Bouet F., Servent D., Molgo J., Menez A., Letourneux
Lancelin J.-M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEEE91969BF5E5BD CRC64;
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Pred. No. 8.5e+02;
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21-JUL-1986 (Rel. 01, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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1548 MW;
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les 3; Conserv
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Luo S., Kulak J.M., Cartier G.E., Jacobsen R.B., Yoshikami D.,
                                                                                                                                                                                                                                                                                                                                        Biol. Chem. 275:8680-8685(2000).
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100.0%; Pre
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PDB; 1MXN; 30-DEC-02.
PDB; 1MXP; 30-DEC-02.
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nes 3; Conserv
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CXA1_CONAL
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Conus betulinus (Beech cone).
Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
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Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
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-!- MASS SPECTROMETRY: MW=1642.5; METHOD=MALDI.
-!- SIMILARITY: BELONGS TO THE M-SUPERFAMILY OF CONOTOXINS.
                                                                                                                                                                                         Score 23; DB 1; Length 14;
Pred. No. 8.5e+02;
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J. Nat. Toxins 8:341-349(1999).
-!- SUBCELIULAR LOCATION: Secreted.
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                                                                                                                                   AMIDATION.
DEEE91898BF5E5BD CRC64;
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Pred. No. 9.1e+02;
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HSSP; P56973; 1B45.
Postsynaptic neurotoxin; Neurotoxin; Toxin;
Acecylcholine receptor inhibitor; Amidation.
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15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Alpha-conotoxin AuIB.
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PROBABLE.
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MEDLINE=99003392; PubMed=9786965;
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2 12
6 13
15 AA; 1650 MW;
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nes 3; Conserv
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CELPC 6
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Olivera B.M., McIntosh J.M.,
"Alpha-conotoxin AuIB selectively blocks alpha3 beta4 nicotinic acetylcholine receptors and nicotine-evoked norepinephrine release.", J. Neurosci. 18:8571-8579(1998).
                                                                                                                                                   MEDLINE=20187585; PubMed=10722709; Cho J.H., Park K.H., Han K.H.; Cho J.H., Mok K.H., Olivera B.M., McIntosh J.M., Park K.H., Han K.H.; "Nuclear magnetic resonance solution conformation of alpha-conotoxin AuIB, an alpha(3) beta(4) subtype-selective neuronal nicotinic acceptor antagonist.";
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MEDLINE=99003392; PubMed=9786965;
MEDLINE=99003392; Cattier G.B., Jacobsen R.B., Yoshikami D.,
Olivera B.M., McIntosh J.M.;
"Alpha-conotoxin AulB selectively blocks alpha3 beta4 nicotinic
acetylcholine receptors and nicotine-evoked norepinephrine release.";
J. Neurosci. 18:8571-8579(1998).
-!- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they
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Neogastropoda; Conoidea; Conidae; Conus.
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Comus aulicus (Court cone).
Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
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Acetylcholine receptor inhibitor, Amidation, 3D-structure.
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Pred. No. 9.1e+02;
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15 AA; 1578 MW; 84EFE95FDC700155 CRC64;
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IISSUE=Venom;
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bind to the nicotinic acetylcholine receptors (nachR) and thus inhibit them. This peptide blocks mammalian nicotinic acetylcholine receptors composed of alpha-3/beta-4 subunits.
--- SUBCELLULAR LOCATION: Secreted.
--- TISSUB SPECTROITY: Expressed by the venom duct.
--- MASS SPECTROMETRY: MW=1725.6; METHOD=Electrospray.
--- SIMILARITY: Belongs to the conotoxin A-superfamily. Alpha-type
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                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conus aulicus (Court cone).

Bukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
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1E310D3B8FDC7001 CRC64;
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16 16 AMIDATION.
16 AA; 1731 MW; 1E310FEB8FDC7001 CRC64;
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15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Alpha-conotoxin AulC.
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HSSP; P50984; IPRN
Poetsynaptic neurotoxin; Neurotoxin; Toxin;
Acetylcholine receptor inhibitor; Amidation.
                                                                                                                                                             PIR; A59045; A59045.
HSSP, P50984, IPEN.
Postsynaptic eurotoxin; Neurotoxin; Toxin;
Acetylcholine receptor inhibitor; Amidation
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Matches 3; Conserv
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Best Local Similarity
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SEQUENCE
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CXA3_CONAL
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x-RAY CRYSTALLOGRAPHY (1.1 ANGSTROMS).

MEDLINE=96311277; PubMed=8740364;
Martin J.L.;
Amatin J.L.;
Amatin J.L.;
The Torystal structure of the neuronal acetylcholine receptor antagonist, alpha-conotoxin PnIA from Conus pennaceus.";
Tructure 4:417-423(1996).
Structure 4:417-423(1996).
I. Structure 4:417-423(1996).
I. Structure A:417-423(1996).
II Structure A:417-42
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    -i- TISSUE SPECIFICITY: Expressed by the venom duct.
    -i- SIMILARITY: Belongs to the conotoxin A-superfamily. Alpha-type

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Eukaryota, Metazoa, Mollusca, Gastropoda, Orthogastropoda,
Apogastropoda, Caenogastropoda, Sorbeoconcha, Hypsogastropoda,
Neogastropoda, Conoidea, Conidae, Conus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fainzilber M., Hasson A., Oren R., Burlingame A.L., Gordon D., Spira M.E., Zlotkin E., "New mollusc-specific alpha-conotoxins block Aplysia neuronal
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41, Last annotation update)
16 AA
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Biochemistry 33:9523-9529(1994).
                                                                                  (Rel. 34, Created)
(Rel. 34, Last seq
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    STANDARD;
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Best Local Similarity
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01-OCT-1996 (Rel.
28-FEB-2003 (Rel.
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Conservative

15 PPC 17

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PPC 8

Job time : 15 secs

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MEDLINE=9744432; PubMed=929851;
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MEDLINE=98851; PubMede=98851;
MEDLINE=9885
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Acetylcholine receptor inhibitor; Amidation; Sulfation; 3D-structure.
DISULFID 2
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Apogastropoda, Caenogastropoda, Sorbeoconcha, Hypsogastropoda,
Neogastropoda, Conoidea, Conidae, Conus.
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Fainzilber M., Hasson A., Oren R., Burlingame A.L., Gordon D.,
Spira M.E., Zlockin E.;
"New mollusc-specific alpha-conotoxins block Aplysia neuronal
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01-0CT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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AMIDATION.
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J. Mass Spectrom. 34:447-454(1999).
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Conus pennaceus (Feathered cone).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          acetylcholine receptors.";
Biochemistry 33:9523-9529(1994).
                                                     STANDARD;
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PDB; 1AKG; 20-MAY-98.
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Gaps . 0 23.0%; Score 23; DB 1; Length 16; 100.0%; Pred. No. 9.7e+02; Live 0; Mismatches 0; Indels Query Match Best Local Similarity 100.v, 3; Conservative

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PPC 8

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Search completed: September 5, 2004, 10:54:59

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RESULT 1	10 00007E	AC 080GZ5;	DT 01-JUN	DT 01-JU	DT 01-JUN	DE Guanir	GN GNAO.	OS Fugu 1								-			_		-	-				SQ SEQUENCE	Query Match	Matchee		٥'n

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Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.; Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.; Sequence variation and physical state of human Papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia."; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AF407221; AAL01409.1;
                                                                                                                                                                                                                                                                                          Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.; Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.; Squence variation and physical state of human Papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia."; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AF407217; AL01397.1; -. NON_TER
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Pred. No. 1.3e+03;
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
NCBI_TaxID=10581;
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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STRAIN=HPV16E2CC6;
Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
"Sequence variation and physical state of human Papillomavirus type 16
"Sequence variation and physical state of human Papillomavirus type 16
cervical cancer isolates from Australia and New Caledonia.";
submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
BMBL, AF407219; AAL01403.1; -.
NON_TER
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Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
"Sequence variation and physical state of human Papillomavirus type 16
"Sequence variation and physical state of human Papillomavirus type 16
Sequence variation and blosses isolates from Australia and New Caledonia.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF407220; AAL01406.1; -.
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
                                                                                                                                                                                                                                                                      El protein (Fragment).
El D.
Human papillomavirus type 16.
Viruses, dsDNA viruses, no RNA stage, Papillomaviridae;
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                                                                                                                                                                          (TrEMBLrel. 19, Created)
(TrEMBLrel. 19, Last sequence update)
(TrEWBLrel. 19, Last annotation update)
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                                                                                                                   PRT;
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01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
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Best Local Similarity
Matches 6; Conserv
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Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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NCBI_TaxID=10581;
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NCBI_TaxID=10581;
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Q918T4;
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Q918T6
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                                                    RESULT 2
091814
1D 091814
1D 09180
DT 01-D
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"Characterization of Claviceps species pathogenic on Borghum by sequence analysis of the beta-tubulin gene intron 3 region and EF1-alpha gene intron 4.";

Mycologia 93:541-551(201)

EMBL; AF255889; AAK37634.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN=Clp-1, and Clp-2; Tooley P.W., Goley E.D., Carras M.M., Frederick R.D., Weber E.L., Kuldau G.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claviceps purpurea (Ergot fungus).

Eukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes;

Hypocreomycetidae, Hypocreales, Clavicipitaceae, Claviceps.
                                                                                                     Length 16;
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Pred. No. 1.3e+03;
2; Mismatches 1; Indels
                                                                                                                                        1; Indels
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
                                                           2C7D73A03A17965F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE 16 AA; 1710 MW; 2C7D73A03A17965F CRC64;
                                                                                                                                                                                                                                                                                                                                              01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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Last annotation update)
                                                                                               Score 26; DB 12;
Pred. No. 1.3e+03;
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                                                       16 AA; 1710 MW;
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ilarity 54.5%;
Conservative
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54.5%;
                EMBL; AF407216; AAL01394.1;
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Best Local Similarity 54.5
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CVS--GQNTNT 15
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                                                                     STRAIN=HPV16E2CC5;
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SEQUENCE
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Q9C0S9
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"Sequence variation and physical state of human Papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF407214; AAL01388.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.,
"Sequence variation and physical state of human Papillomavirus type 16
cervical cancer isolates from Australia and New Caledonia.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF407215; AAL01391.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.; "Sequence variation and physical state of human Papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia."; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
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Pred. No. 1.3e+03;
2; Mismatches 1; Indels
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
                                                                                                                                                                       SEQUENCE 16 AA; 1710 MW; 2C7D73A03A17965F CRC64;
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(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
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54.5%;
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01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
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                                          STRAIN=HPV16E2CC1;
                    SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-HPV16E2CC2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Papillomavirus.
NCBI_TaxID=10581;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. STRAIN=HPV16E2CC3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10581;
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01-DEC-2001
01-DEC-2001
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Conservative
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Best Local Similarity
Local 5; Conserv?
                                                                                                                 8 AAELGKGS 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Elongation factor.
NON TER 1
NON TER 17
SEQUENCE 17 AA;
                                                                                          2 ASELGKST 9
                                              Query Match
Best Local Similarity
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NON TER
NON TER
SEQUENCE
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Q9C0S7;
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Q8NIJ6
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                                                                     Matches
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Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AY043480; AAK95396.1; -.

EMBL; AY043481; AAK95396.1; -.

GD; GO:0003746; F:translation elongation factor activity; IEA.

Elongation factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                      Gaps
                                                                                                                                                                                                                                                                                          STRAIN=Cla-2, Cla-7, Cls-1, and Cls-2;
Tooley P.W., Goley B.D., Carras M.M., Frederick R.D., Weber B.L.,
Kuldau G.A.,
Edwardterization of Claviceps species pathogenic on sorghum by
sequence analysis of the beta-tubulin gene intron 3 region and EF1-
alpha gene intron 4.";
Mycologia 93:541-551(201),
EMBL; AF255899; AAX37641.1;
EMBL; AF255899; AAX37643.1;
EMBL; AF255899; AAX37641.1;
EMBL; AF255899; AAX37641.1;
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Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.
NCBI_TaxID=169388;
                                      ;
                                                                                                                                                                                                                                   Eukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes, Hypocreomycetidae, Hypocreales, Clavicipitaceae, Claviceps. NCBI_TaxID=83212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 17;
               26.0%; Score 26; DB 3; Length 17;
62.5%; Pred. No. 1.4e+03;
live 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                       17 17 AA; 1911 MW; 110075F1817FF1D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
Translation elongation factor 1 alpha (Fragment).
Fusarium solani.
                                                                                                                                                                01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 26; DB 3; I
Pred. No. 1.4e+03;
                                                                                                                                              17 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 62.5
Matches 5; Conservative
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                                                               2 ASELGKST 9
                                                                                                                                                                                                                              Claviceps africana.
                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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Q9C0S6
                                         Matches
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Li S.;
"Molecular characterization of Fusarium solani f. sp. glycines based
on the translation elongation factor 1-alpha gene.";
submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF39645; AAM73735.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Claviceps sorghicola.
Claviceps Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Bukaryota; Fungi; Ascomycota; Clavicipitaceae; Claviceps.
Hypocreomycetidae; Hypocreales; Clavicipitaceae; Claviceps.
NCBI_TaxID=83213;
                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
17-Instalation elongation factor 1-alpha (Fragment).
Fusarium solani f. 8p. glycines.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.
1011 TaxID=108887;
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EMBL; AR395654; AAM73744.1; --
EMBL; AR395655; AAM73745.1; --
EMBL; AF395655; AAM73746.1; --
EMBL; AF395657; AAM73746.1; --
EMBL; AR395657; AAM73747.1; --
EMBL; AR395657; AAM73747.1; --
EMBL; AR395667; Etranslation elongation factor activity; IEA.
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                                                                                             Length 17;
                                                                                     Score 26; DB 3; Length 17; Pred. No. 1.4e+03; 2; Mismatches 1; Indels
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17 17
17 AA; 1911 MW; 110075F1817FF1D9 CRC64;
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Last annotation update)
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EMBL; AF395647; AAM7373.1;
EMBL; AF395648; AAM73738.1;
EMBL; AF395649; AAM73740.1;
EMBL; AF395650; AAM73740.1;
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                                                                                               26.0%;
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WE SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN-6/3ap-2, and Cjap-4;

Tooley P.W., Goley B.D., Carras M.M., Frederick R.D., Weber E.L.,

Kuldau G.A.,

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SEQUENCE FROM N.A.
STRAIN-Cpas-1, and Cpas-2;
TOOley P.W., Goley B.D., Carras M.M., Frederick R.D., Weber E.L.,
Tooley P.W., Goley E.D., Carras M.M., Frederick R.D., Weber E.L.,
Tooley P.W., Goley B.D., Carras M.M., Frederick R.D., Weber E.L.,
Ruldau G.A.;
"Characterization of Claviceps species pathogenic on sorghum by
sequence analysis of the beta-tubulin gene intron 3 region and EFI-
alpha gene intron 4.";
Mycologia 93:541-551(2001).
EMBL; AF255892; AAX376371;
EMBL; AF255893; AAX376371;
EMBL; AF255893; AAX37638.1;
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Clavicipitaceae; Claviceps.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26.0%; Score 26; DB 3; Length 17; 62.5%; Pred. No. 1.4e+03; ative 2; Mismatches 1; Indels
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OPCOS8;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
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8 AAELGKGS 15
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AC 090088
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DT 01-JUD
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GN CIEY1.
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OC HYPOCIO
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Search completed: September 5, 2004, 10:56:03 Job time : 58 secs

8 AAELGKGS 15

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Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine
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Aau04536 VEGF b
Aau06481 Peptid
Aau10122 Human
Aay5139 Feline
Aay95290 Human
Aay5529 RC Se
Aay95290 Human
Aay5529 RC Se
Aay95290 Human
Aay5529 RC Se
Aay9524 Human
Aay562 HIV-1
Aaw43828 HIV-1
Aaw43828 HIV-1
Aaw43828 HIV-1
Aaw4364652 HIV-1
Aaw43674 Cyclic
Aay417381 ARI-1mi
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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                                    OM protein - protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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geneseqp2003bs:*
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1: geneseqp1980s:*
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No.
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Aab46653 HIV-1 Tat Aab46654 HIV-1 Tat Aab08459 Peptide C Abj04094 Immunoglo Aay6672 T cell an Aab46655 HIV-1 Tat Abb24924 HIV DR Su Abb181894 HIV DR Su Aar25715 CB1 partin Aar27142 Peptide f Aar37342 Peptide f Aar4268 Citrus bl Aar46657 HIV-1 Tat Aab46657 HIV-1 Tat Aab2604 T cell an Aab46657 HIV-1 Tat Aab2604 HIV Tat Tat Aab2664 HIV-1 Tat Aab2664 HIV-1 Tat Aab2664 HIV-1 Tat Aab2664 HIV-1 Tat Aab2664 HIV-1 Tat Aab2664 HIV-1 Tat	; ta	blude 1, and m a dimeric appearing as
Aab46 Aab46 Abj09 Abj09 Abj09 Aby66 Abb69 Abr29 Abr29 Abr81 Abr80 Abb88	angiog tumon arthn C.	peptide to for the sequence meric peptide.
AAB46653 AAU08459 AAU04094 AAU04094 AAX66872 AAB46655 AAB46656 ABP24824 AAR25715 AAR25715 AAR25715 AAR25715 AAR1288 AAX66903 AAX66903 AAX66903 AAR81821 AAB81821 AAB25943 AAB25943 AAB46658 AAU6668 AAU6668 AAU16668	17 AA. peptide #1. helial growth giogenesis; ps r sequelae; ri ic inflammatic alifiers s bond cyclise	f an identicator residue 1 so forming a so forming a so forming a second
4 4 4 6 6 6 8 4 4 4 4 6 6 8 8 8 8 8 8 8	standard; protein; 17 AA. 10 (first entry) d bicyclic dimeric peptide GF; vascular endothelial g arisation; lymphangiogenes induced neovascular sequel retinopathy; chronic infla Location/Qualifiers Location/Qualifiers Location/Qualifiers -bond 1. 13 -bond 1. 13	Edue 17 21de, c 24528, 01528, 017629 020459
	standard;] Ol (first d bicyclic GF; vasculi arisation; induced nec retinopath, Loca -bond 1bond 1	res: pepp padu 55-A1. 11. 201000 10; 2000US- 10; 2000US- 10; 2000US- 10; 2000US-
3 3 3 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	U04	WO200152875-A1. 26-JUL-2001. 18-JAN-2001; 20 16-MAY-2000; 20 (LUDM-) LUDWIG
	A A A A A A A A A A A A A A A A A A A	FFFXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX

Cendron A;

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method of producing a monomeric monocyclic peptides by a meabling beta-
ce beta carbon separation distances on opposite antiparallel strands of a
ceptide loop fragment from an exposite antiparallel strands of a
cyclising the peptide by oxidiaing the cysteine residues. The monocyclic
cyclising the peptide by oxidiaing the cysteine residues. The monocyclic
cyclisation are used to interfere with anglogenesis.

Cyclisation are used to independent to impure a condition

Cyclisation are used to independent to interfere permeability

Cyclisation and the mamman has a condition characterised by fluid

Cyclisation in peripheral limbs or in lungs, peritoneal cavity, pleura,

Cyclisation are used to image blood vessels and lymphatic

Cyclisation independent permeability induced by VEGF. VEGF-C or -D and

Cyclisation in the peptides are used to incerfere

Cyclisation in combination with an anti-inflammatory agent, to treat a

Cyclisation inflammation, especially rheumatoid arthritis, psoriasis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "A disulfide bond forms between residue 17 and residue 1 of the sequence appearing as AAU04528, forming a dimeric peptide"
                 whose 3-dimensional structure is modelled on the expose loop of human VEGFD (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring beta-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
sequence represents a dimeric bicyclic peptide of the invention,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 100; DB 4; Length 17; 100.0%; Pred. No. 6.2e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels

    .13
    /note= "This bond cyclises the peptide"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VEGF based bicyclic dimeric peptide #7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU04550 standard; peptide; 17 AA.
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16-MAY-2000; 2000US-0204590P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.
Best Local Similarity 100.
Matches 17, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         diabetic retinopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disulfide-bond
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The sequence represents a dimeric bicyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human whose 3-dimensional structure is modelled on the expose loop of human configuration relates to a method of producing a monomeric monocyclic peptide by a measuring beta-configuration of producing a monomeric monocyclic peptide by a measuring beta-configuration the peptide by oxidising the exposed loop of a growth factor protein and cyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior conclisation are used to interfere with angiogenesis, conclisation are used to interfere with angiogenesis, conclisation are used to interfere with angiogenesis, conclisation is diabetic retinopathy, postiast, atthropathy cerebrovascular accident, post-angioplasty restenosis, head, heat or condition is diabetic retinopathy, postiast, post-angioplasty restenosis, head, heat or cold trauma, substance-induced neovascularisation of the liver, excessive corporated angiogenic dysfunction, diabetes induced neovascular sequelae, hypertension induced neovascular sequelae, or chronic liver infection. The peptides are also used to modulate vascular permeability in a communation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain. The peptides are used to image blood vessels and lymphatic corputation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain. The peptides are used to image blood vessels and lymphatic corputation inflammation with an anti-inflammatory agent, to treat a christian continuous expecially rheumatoid arthritis, psoriasis and continuous corputation inflammation with an anti-inflammatory agent, to treat a christian continuous continuous
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                                                                                                                        Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vascular endothelial growth factor; angiogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           neovascularisation; lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97.0%; Score 97; DB 4; Length 1/; 94.1%; Pred. No. 1.7e-07; Office of Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ä
                                            Cendron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VEGF based bicyclic dimeric peptide #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                            Example 26; Page 49; 102pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ä.
                                              Stacker S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU04546 standard; peptide; 17
(LUDW-) LUDWIG INST CANCER RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 94.1
les 16; Conservative
                                              Hughes RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diabetic retinopathy
                                                                                        WPI; 2001-442248/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-SEP-2001
                                              Achen MG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU04546;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                       residues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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/note= "A disulfide bond forms between residue 17 and residue 17 of an identical peptide to form a dimeric peptide"

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(LUDW-) LUDWIG INST CANCER RES
                   18-JAN-2001; 2001WO-US001533.
                        18-JAN-2000; 2000US-0176293P.
16-MAY-2000; 2000US-0204590P.
         WO200152875-A1
               26-JUL-2001.
                                     Achen MG,
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Cendron A;

Stacker S,

Hughes RA,

The sequence represents a dimeric bicyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human CC whose 3-dimensional structure is modelled on the expose loop of human CC whose 3-dimensional structure is modelled on the expose loop of human CC wearly (ascular endothelial growth factor). The invention relates to a beta carbon separation distances on opposite antiparallel strands of a peptide loop fragment from an exposed loop of a growth factor protein and CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with angiogenesis, concarterised by angiogenesis, neovascularisation or lymphangiogenesis in neovascularisation or lymphangiogenesis. The condition is diabeted retrinopathy, psoriasis, arthropathy, hemangioma, vascularised malignant or benign tumour, post-recovery creatms, substance-induced neovascularisation of the liver, excessive cerebrovascular accident, post-amignoplasty restenosis, head, heat or claumer with a substance-induced neovascular sequelae, or chronic liver creams, substance-induced neovascular sequelae, or chronic liver confiction. The peptides are also used to modulate vascular permeability accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain. The peptides are used to image blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are used to interfere with at least one biological activity induced by VBGF. Cor -D and charant inflammatory agent, to treat a chabetic retinant. Gaps diabetic retinopathy Similarity Sequence 17 AA;

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0
97.0%; Score 97; DB 4; Length 17; 94.1%; Pred. No. 1.7e-07; 1ve 1; Mismatches 0; Indels
                               Conservative
                               16;
 Query Match
Best Local 9
                             Matches
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17 17 CASELGKSTNTFCKPPC

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AAU04547 standard; peptide; 17 AA. AAU04547;

RESULT 4 AAU04547

(first entry) 26-SEP-2001 EXXXXEX

o;

Gaps

·: 0

Length 17; Indels

Score 93; DB 4; Len Pred. No. 6.9e-07;

93.0%; 88.2%;

Query Match 93.0 Best Local Similarity 88.2 Matches 15; Conservative

chronic inflammation, especially rheumatoid arthritis, psoriasis and

diabetic retinopathy

Sequence 17 AA;

Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine Example 26; Page 49; 102pp; English WPI; 2001-442248/47. residues

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The adjustic reptresents a uniment with the expose loop of human whose 3-dimensional structure is modelled on the expose loop of human unetained of producing a monomeric monocyclic peptide by a measuring betact beta carbon separation distances on opposite antiparallel strands of a peptide loop fragment from an exposed loop of a growth factor protein and peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior or cyclisation are used to interfere with angiogenesis.

CC cyclisation are used to interfere with angiogenesis.

CC cyclisation are used to interfere with angiogenesis.

CC chevacaterised by angiogenesis, neovascularisation or lymphangiogenesis.

CC checkind angiogenesis, neovascularisation or lymphangiogenesis.

CC recebrovascular accident, post-angioplasty restenosis, arthropathy.

CC recebrovascular accident, post-angioplasty restenosis, anthropathy.

CC recebrovascular accident, post-angioplasty restenosis, head, heat or cold trauma, substance-induced neovascular sequelae, or chronic liver consistent accident, post-angioplasty restenosis in fuduced neovascular sequelae, or chronic liver consistent infection. The peptides are also used to modulate vascular permeability in a mammal (the mammal has a condition characterised by fluid accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain. The peptides are also used to modulate vascular permeability vascularing the mammal has a condition characterised by fluid accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain. The peptides are used to image blood vessels and lymphatic vascular and himperipheral and himper priparent condition and himperipheral manner present to image to imag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vasculature. The monomeric and bicyclic peptides are used to interfere with at least one biological activity induced by VEGF, VEGF-C or -D and are also used in combination with an anti-inflammatory agent, to treat a
                                                                                                                                                                                                                                                                                                                                   /note= "A disulfide bond forms between residue 17 and residue 17 of an identical peptide to form a dimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence represents a dimeric bicyclic peptide of the invention,
                                                   Human, VBGF; vascular endothelial growth factor; angiogenesis; neovascularisation; lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic.

    .13
/note= "This bond cyclises the peptide"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cendron A;
  VEGF based bicyclic dimeric peptide #4.
                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 26; Page 49; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stacker S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (LUDW-) LUDWIG INST CANCER RES
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16-MAY-2000; 2000US-0204590P.
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                                                                                                                                                                                                                                                                                                                                                                                               peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hughes RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-442248/47.
                                                                                                                                                                                                                                                        Disulfide-bond
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                                                                                                                                                                                  Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "A disulfide bond forms between residue 17 and residue 1 of the sequence appearing as AAU04528, forming a dimeric peptide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; VEGF; vascular endothelial growth factor; angiogenesis; neovascularisation; lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic.

    .13
/note= "This bond cyclises the peptide"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VEGF based bicyclic dimeric peptide #8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 26; Page 49; 102pp; English.
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                                                                                                                                                                                                                                                            AAU04551 standard; peptide; 17 AA
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       CASELGKSTNTFCKPPC 17
                                            1 CASELGKTSNTFCKPPC 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-JAN-2000; 2000US-0176293P.
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                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-442248/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200152875-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                        26-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Achen MG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           residues.
                                                                                                                                                                                                                                                                                                                                         AAU04551;
              ч
                                                                                                                                                                                             RESULT
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The sequence represents a dimeric bicyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human VEGFD (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring betabete carbon separation distances on opposite antiparallel strands of a peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
                                                                                                                                                                                                          ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine
or brain. The peptides are used to image blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are used to interfere with at least one biological activity induced by VBGF. VEGF-C or -D and are also used in combination with an anti-inflammatory agent, to treat a chronic inflammation, especially rheumatoid arthritis, psoriasis and
                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note= "A disulfide bond forms between residue 17 and residue 17 of an identical peptide to form a dimeric
                                                                                                                                                                                                          ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; VEGF; vascular endothelial growth factor; anglogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      neovascularisation; lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic.
                                                                                                                                                                         Length 17;
                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "This bond cyclises the peptide"
                                                                                                                                                                       93.0%; Score 93; DB 4; I
88.2%; Pred. No. 6.9e-07;
iive 2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cendron A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VEGF based bicyclic dimeric peptide #6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 26; Page 49; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                              AAU04549 standard; peptide; 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-JAN-2000; 2000US-0176293P.
16-MAY-2000; 2000US-0204590P.
                                                                                                                                                                                                                                                  17
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                                                                                                                                                                                                                                                                                1 CASÉLGRSTNSFCKPPC 17
                                                                                                                                                                                                                                                  1 CASELGKSTNTFCKPPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 peptide"
                                                                                                                                                                                                                 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-442248/47
                                                                                                     diabetic retinopathy
                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Digulfide-bond
                                                                                                                                         Sequence 17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200152875-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                  AAU04549;
                                                                                                                                                                           Query Match
                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                             RESULT 6
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to oyclisation are used to interfere with angiogenesis,

neovascularisation or lymphangiogenesis in a mammal with a condition

characterised by angiogenesis, neovascularisation or lymphangiogenesis.

The condition is diabetic retinopathy, psoriasis, arthropathy,

the condition is diabetic retinopathy, psoriasis, arthropathy,

cerebrovascular accident, post-angioplasty restenosis, head, heat or cold

trauma, substance-induced neovascularisation of the liver, excessive

formone-related angiogenic dysfunction, diabetes induced neovascular

confection. The peptides are also used to modulate vascular permeability

in a mammal (the mammal has a condition characterised by fluid

corumulation in peripheral limbs or in lurgs, peritoneal cavity, pleura,

or brain. The peptides are used to image blood vessels and lymphatic

vasculature. The monomeric and bicyclic peptides are used to interfere

covasculature. The monomeric and bicyclic peptides are used to interfere

covasculature. The monomeric and bicyclic peptides are used to interfere

covasculature, and bicyclic peptides are used to interfere

covasculature, and bicyclic peptides are used to confinenter of chronic inflammation, especially rheumatoid arthritis, psoriasis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
and a cyclic peptide with at least one amino acid deleted prior
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "A disulfide bond forms between residue 17 and residue 17 of an identical peptide to form a dimeric
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; VEGF; vascular endothelial growth factor; angiogenesis; neovascularisation; lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                Score 93; DB 4; Length 17;
Pred. No. 6.9e-07;
2; Mismatches 0; Indels

    13
    /note= "This bond cyclises the peptide"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VEGF based bicyclic dimeric peptide #5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU04548 standard; peptide; 17 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stacker S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (LUDW-) LUDWIG INST CANCER RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CASELGKSTNTFCKPPC 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CASELGRSTNSFCKPPC 17
                                                                                                                                                                                                                                                                                                                                                                                                                93.0%;
88.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-JAN-2000; 2000US-0176293P.
16-MAY-2000; 2000US-0204590P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-JAN-2001; 2001WO-US001533.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Achen MG, Hughes RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-442248/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                         Sequence 17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disulfide-bond
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                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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from an exposed loop of a growth factor protein by oxidizing the cysteine
                                                                                                                                                                                        peptide loop fragment from an expense anti-paratic actains of a cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with angiogenesis. The movascularisation or lymphangiogenesis in a mammal with a condition characterised by angiogenesis, neovascularisation or lymphangiogenesis. The condition is diabetic retinopathy, postciasis, arthropathy, hemangioma, vascularised malignant or benign tumour, post-recovery cerebrovascular accident, post-angioplasty restenosis, head, heat or cold trauma, substance induced meovascularisation of the liver, excessive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vasculature. The monomeric and bicyclic peptides are used to interfere with at least one biological activity induced by VEGF, VEGF-C or -D and are also used in combination with an anti-inflammatory agent, to treat a chronic inflammation, especially rheumatoid arthritis, psoriasis and diabetic retinopathy
                                                                                                                                                                                                                                                                                                                                                                                                        hormone-related angiogenic dysfunction, diabetes induced neovascular sequelae, hypertension induced neovascular sequelae, or chronic liver infection. The peptides are also used to modulate vascular permeability in a mammal (the mammal has a condition characterised by fluid accumulation in peripheral limbs or in lungs, periconeal cavity, pleura, or brain. The peptides are used to image blood vessels and lymphatic
                                                                                                                   whose 3-dimensional structure is modelled on the expose loop of human VEGFD (vascular endothellal growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring betabeta carbon separation distances on opposite antiparallel strands of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                   sequence represents a dimeric bicyclic peptide of the invention,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; VEGF; vascular endothelial growth factor; angiogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             neovascularisation; lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 89; DB 4; Length 17, Pred. No. 2.7e-06;

    .13
/note= "This bond cyclises the peptide"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diabetic retinopathy; chronic inflammation; cyclic.
                                                        Example 26; Page 49; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU04524 standard; peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VEGF based monocyclic peptide 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CASELGKSTNTFCKPPC 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CASDVGKSTNTWCKPPC 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-JAN-2001; 2001WO-US001533.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89.08;
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16-MAY-2000; 2000US-0204590P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disulfide-bond
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-JUL-2001.
                        residues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 8
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18-JAN-2001; 2001WO-US001533

WO200152875-A1.

26-JUL-2001

Cendron A;

Stacker S,

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The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human vacable (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring betact composition of producing a monomeric monocyclic peptide by a measuring betact composition the peptide by oxidising the peptide a growth factor protein and cyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior or cyclisation are used to interfere with angiogenesis.

CC peptides, dimeric bicyclic peptide with at least one amino acid deleted prior corpitation are used to interfere with angiogenesis.

CC peptides, and a cyclic peptide with at least one amino acid deleted prior corpitation are used to interfere with angiogenesis.

CC recipitation or lymphangiogenesis in a mammal with a condition characterised by angiogenesis, neovascularisation or lymphangiogenesis.

CC reciprovascular accident, post-angioplasty restenosis, head, heat or cold cramma, substance-induced neovascularisation of the liver, excessive corpitation in peripheral limps or in lungs, peritoned neovascular sequelae, hypertension induced neovascular sequelae, hypertension induced neovascular sequelae, hypertension induced neovascular sequelae, or chromic liver corputation in peripheral limps or in lungs, peritoneal cavity, pleura, or brain. The peptides are also used to induced neovascular accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain. The peptides are used to image blood vessels and lymphatic compination with an anti-inflammatory agent, to treat a chronic inflammation, especially rheumatoid arthritis, psoriasis and contrains and contrains are used to interfere contrains and peripheral activity induced by VEGF, VEGF, Cor D and are also used in combination with an anti-inflammatory agent, to treat a contrain contrains and peripheral act
                                                                                                                                                                                         Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine
                                                                                                                                                                                                                                                                                                                                                          Claim 49; Page 32; 102pp; English.
                      (LUDW-) LUDWIG INST CANCER RES
                                                                                     Hughes RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diabetic retinopathy
                                                                                                                                             WPI; 2001-442248/47
                                                                                        Achen MG,
                                                                                                                                                                                                                                                                                                        residues.
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Gaps ö Score 72; DB 4; Length 13; Pred. No. 0.00073; 0; Indels 72.0%; Scor. 100.0%; Pred. No. v. 0; Mismatches 1 CASELGKSTNIFC 13 1 CASELGKSTNTFC 13 Matches 13; Conservative Query Match Best Local Similarity à g

Sequence 13 AA;

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AAU04534 standard; peptide; 13 AA. 26-SEP-2001 (first entry) AAU04534; RESULT 9 AAU04534

VEGF based monocyclic peptide 12.

Human; VEGF; vascular endothelial growth factor; angiogenesis; neovascularisation; lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic.

Synthetic

 .13 /note= "This bond cyclises the peptide" Location/Qualifiers Disulfide-bond

The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human VEGFD (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring beta carbon separation distances on opposite antiparallel strands of a peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine Cendron A; Example 25; Page 47; 102pp; English. Achen MG, Hughes RA, Stacker S, (LUDW-) LUDWIG INST CANCER RES 18-JAN-2000; 2000US-0176293P. 16-MAY-2000; 2000US-0204590P. diabetic retinopathy WPI; 2001-442248/47. residues

.. 0 Score 69; DB 4; Length 13; Pred. No. 0.002; 1; Mismatches 0; Indels ; 69.0%; 92.3%; Query Match
Best Local Similarity 92.3
....hes 12; Conservative Sequence 13 AA;

. 0

Gaps

13 1 CASELGKSTNTFC CATELGKSTNTFC

> ઠે d

RESULT 10

AAU04535 standard; peptide; 13 AA. VEGF based monocyclic peptide 13. (first entry) 26-SEP-2001 AAU04535; AAU04535 **XXEXEXEX**

Human; VEGF; vascular endothelial growth factor; angiogenesis;

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The sequence represents a monomeric monocyclic peptide of the invention, whose 3 dimensional structure is modelled on the expose loop of human vEGFD (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring beta beta carbon separation distances on opposite antiparallel strands of a peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides, dimeric bicyclic peptide (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior conception are used to interfere with angiogenesis, neovascularisation or lymphangiogenesis in a mammal with a condition characterised by angiogenesis, neovascularisation or lymphangiogenesis, The condition is diabetic retinopathy, psoriasis, arthropathy, post-recovery carbonare and a condition of the period of the condition of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cerebrovascular accident, post-angioplasty restenosis, head, heat or cold trauma, substance-induced neovascularisation of the liver, excessive hormone-related angiogenic dysfunction, diabetes induced neovascular sequelae, hypertension induced neovascular sequelae, or chronic liver infection. The peptides are also used to modulate vascular permeability accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain. The peptides are used to image blood vessels and lymphatic or brain. The poptides are used to image blood vessels and lymphatic with at least one biological activity induced by VEGF. VEGF-C or -D and are also used in combination with an anti-inflammatory agent, to treat a sinceric continuation, especially rheumatoid arthritis, psoriasis and although and arthritis, psoriasis and
neovascularisation; lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis;
                                 diabetes induced neovascular sequelae, rheumatoid a diabetic retinopathy; chronic inflammation; cyclic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 25; Page 47; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (LUDW-) LUDWIG INST CANCER RES
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                                                                                                                                                                                                                         Disulfide-bond
                                                                                                                                                                                                                                                                                                                             WO200152875-A1
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                                                                                                                                                                                                                                                                                                                                                                                             26-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Achen MG,
                                                                                                                                  Synthetic
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Length 13; Indels . 0 65.0%; Score 65; DB 4; 84.6%; Pred. No. 0.008; 2; Mismatches Local Similarity 84.6 Query Match Matches 8

Gaps 0; 1 CASELGKSTNTFC 13

ô 1 CASELGKTSNTFC 13

RESULT 11 AAU04537

vascular endothelial growth factor; angiogenesis; neovascularisation; lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic. AAU04537 standard; peptide; 13 AA. VEGF based monocyclic peptide 15. (first entry) 26-SEP-2001 Synthetic AAU04537; Human;

.13 /note= "This bond cyclises the peptide"

Location/Qualifiers

 .13 /note= "This bond cyclises the peptide" Location/Qualifiers Key Disulfide-bond

WO200152875-A1.

Cendron A;

Hughes RA, Stacker S,

26-JUL-2001

18-JAN-2001; 2001WO-US001533.

18-JAN-2000; 2000US-0176293P. 16-MAY-2000; 2000US-0204590P.

(LUDW-) LUDWIG INST CANCER RES

Cendron A; Stacker S, Hughes RA, Achen MG,

WPI; 2001-442248/47.

Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine

Example 25; Page 47; 102pp; English.

or cold

The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human vegeb (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring betabeta carbon separation distances on opposite antiparallel strands of a beta carbon separation distances on opposite antiparallel strands of a cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides, dimeric bicyclic peptide with at least one amino acid deleted prior cyclising the peptide with at least one amino acid deleted prior cyclisation are used to interfere with angiogenesis.

CC draracterised by angiogenesis, neovascularisation or lymphangiogenesis.

CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.

CC crebrovascular accident, post-angioplasty restenosis, head, heat or clauma substance-induced neovascularisation of the liver, excessive or frauma, substance-induced neovascularisation of the liver, excessive or frauma, substance-induced neovascularisation of the liver accumulation in peripheral limbs or in lungs, peritoneal cavity, accumulation in peripheral limbs or in lungs, peritoneal cavity, accumulation in peripheral limbs or in lungs, peritoneal cavity, accumulation in peripheral limbs or in lungs, peritoneal cavity, accumulation in peripheral activity induced by VEGF-C or D and characterised by Apperience of chronic inflammation with an anti-inflammatory agent, to treat a charinomark. diabetic retinopathy

AA;

Length 13; Score 65; DB 4; Pred. No. 0.008; 65.0**%**; 84.6**%**; Query Match Best Local Similarity -D and treat a

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Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200162942-A2
                                                                                     Sequence 13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                        21-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                       AAU08482;
                                                                                                                                                                                                                                                                                                   RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human vacable to a vector of producing a monomeric monocyclic peptide by a measuring beta-cc beta carbon separation distances on opposite antiparallel strands of a cyclishing the peptide by oxidaing the exposed loop of a growth factor protein and cyclisting the peptide by oxidaing the exposed loop of a growth factor protein and cyclisation are used to interfere with a least one amino acid deleted prior peptides, and a cyclic peptide with at least one amino acid deleted prior cyclisation are used to interfere with angiogenesis, concaularisation or lymphangiogenesis in a mammal with a condition characterised by angiogenesis, neovascularisation or lymphangiogenesis. The condition is diabetic retinopathy, psoriasis arthropathy, corebrovascular accident, post-angioplasty restenosis, head, heat or cold trauma, substance-induced neovascularisation of the liver, excessive corporation induced neovascular sequelae, or chronic liver carquelae, hypertension induced neovascular sequelae, or chronic liver infection. The peptides are also used to modulate vascular permeability in a mammal limbs or in lungs, peritoneal cavity, pleura, corbrain. The peptides are used to image blood vessels and lymphatic cor brain. The peptides are used to image blood vessels and lymphatic avaculature. The monomeric and bicyclic peptides are used to interfere
 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine
 Gaps
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                                                                                                                                                                                                                                                                                                                       growth factor; angiogenesis;
                                                                                                                                                                                                                                                                                                                                    neovascularisation, lymphangiogenesis, psoriasis, tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic.
     Indels
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     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stacker S,
                                                                                                                                                                         AAU04536 standard; peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                         vascular endothelial
                                                                                                                                                                                                                                                                                      VEGF based monocyclic peptide 14.
     5,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-JAN-2001; 2001WO-US001533.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-JAN-2000; 2000US-0176293P.
                                                                                                                                                                                                                                                     (first entry)
                                                                1 CASELGRSTNSFC 13
                                          1 CASELGKSTNTFC 13
       11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Achen MG, Hughes RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-442248/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200152875-A1
                                                                                                                                                                                                                                                                                                                             Human; VEGF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-JUL-2001
                                                                                                                                                                                                                                                   26-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      residues
                                                                                                                                                                                                                AAU04536;
         Matches
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The present invention relates to polypeptides that bind cellular receptors for vascular endothelial growth factors (VEGFs), the modulate strateging them, and their use for identifying agents that polynucleotides encoding them, and their receptors VEGFs and their modulate interactions between VEGFs and their receptors play an important role in vasculogenesis, the development of receptors play an important role in vasculogenesis, the development of the embryonic vasculature from early differentiating endothelial cells and analogenesis, the process of forming new blood vessels from presents ingled cancers, abnormal angiogenesis, may be used to treat dysfunction of the endothelial cell regulatory proliferative retinopathies, age-related macular degeneration, rheumatoid arthritis and psoriasis. The polypeptides of the invention exhibit unique arthritis and psoriasis. The polypeptides of the invention exhibit unique acceptors binding profiles compared to known naturally occurring vEGFs. AAU08479-AAU08483 represents peptides which inhibit human VEGF-C mediated activation of VEGFR-3
                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, vascular endothelial growth factor; VEGF-C; vasculogenesis; angiogenesis; blood vessel; cancer; proliferative retinopathy; psoriasis; age-related macular degeneration; rheumatoid arthritis; cardiovascular; VEGFR-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polypeptides that bind cellular receptors for vascular endothelial growth
                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide #4 inhibiting human VEGF-C mediated activation of VEGFR-3.
with at least one biological activity induced by VEGF, VEGF-C or are also used in combination with an anti-inflammatory agent, to chronic inflammation, especially rheumatoid arthritis, psoriasis diabetic retinopathy
                                                                                                                                                                                                                                                                                                                                ٥;
                                                                                                                                                                                                                                                            Length 13;
                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                            Score 61; DB 4;
Pred. No. 0.032;
1; Mismatches
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/note= "Any amino acid"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU08482 standard; peptide; 14 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (LUDW-) LUDWIG INST CANCER RES (LICH) LICENTIA OY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-FEB-2000; 2000US-0185205P.
18-MAY-2000; 2000US-0205331P.
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                                                                                                                                                                                                                                                                    61.0%;
                                                                                                                                                                                                                                                                                                         76.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                               1 CASELGKSTNTFC 13
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CASDVGKSTNTWC 13
                                                                                                                                                                                                                                                                                                                                           10; Conservative
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                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 10; Conser
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Agouti signalling protein; ASP; depigmenting activity; cosmetic; hyperpigmentary condition; melasma photoageing spots; solar keratosis; post-inflammatory hyperpigmentation; wound healing; eumelanogenesis; vitiligo; leucoderma; albinism; hair greying.

96WO-US010695

21-JUN-1996; 23-JUN-1995;

09-JAN-1997.

WO9700892-A2

Human agouti signalling protein fragment #10.

(first entry)

18-SEP-1997

AAW10122;

AAW10122 standard; protein; 10 AA.

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Gaps

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48.0%; Score 48; DB 4; Length 14; 88.9%; Pred. No. 3; 1; Indels.ive 0; Mismatches 1; Indels

|||| ||| TNTFFKPP

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The present invention relates to polypeptides that bind cellular receptors for vascular endothelial growth factors (VEGFs), the polymulate interactions between VEGFs and their teceptors. VEGFs and their modulate interactions between VEGFs and their receptors. VEGFs and their faceptors play an important role in vasculogenesis, the development of the embryonic vasculature from early differentiating endothelial cells and angiogenesis, the process of forming new blood vessels from presents in the process of forming new blood vessels from presents on treat dysfunction of the endothelial cell regulatory system. Such disorders include cancers, abnormal angiogenesis, rhe polypeptides of the invention exhibit unique comparing profiles compared to known naturally occurring VEGFs.
                                                                                                                                                                                                                                                                                                                      Human; vascular endothelial growth factor; VEGF-C; vasculogenesis; angiogenesis; blood vessel; cancer; proliferative retinopathy; psoriasis; age-related macular degeneration; rheumatoid arthritis; cardiovascular; VEGFR-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Polypeptides that bind cellular receptors for vascular endothelial growth factors, polynucleotides encoding them.
                                                                                                                                                                                                                                                                                        Peptide #3 inhibiting human VEGF-C mediated activation of VEGFR-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 64; Page 147; 261pp; English.
                                                                                                                                                                                                      AAU08481 standard; peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (LUDW-) LUDWIG INST CANCER RES. (LICN) LICENTIA OY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-FEB-2001; 2001WO-US006113.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-FEB-2000; 2000US-0185205P.
18-MAY-2000; 2000US-0205331P.
                        Query Match
Best Local Similarity 88.73,
                                                                                                                                                                                                                                                               (first entry)
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                                                                                                    INTECKPPC 17
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               Sequence 14 AA;
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                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                              21-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alitalo K,
                                                                                                    6
                                                                                                                                                                                                                                  AAU08481;
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as
                                                                                                                                                                                                                                                                                                                                                             New agouti signal protein peptide(s) and nucleic acids - used for altering melanin prodn., for treating e.g. melasma photo-ageing spots, solar keratosis or vitiligo.
                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequences given in AAM10101-29 are biologically active peptides a fragments of the agouti signalling protein (ASP) which have depigment activity. These peptides are useful for cosmetic purposes and for clinical application in the prevention or treatment of various hyperpigmentary conditions and diseases such as melasma photoageing spots, solar keratosis, and post-inflammatory hyperpigmentation such occurs at sites of wound healing. They can also be used to provide enhanced equal and active treating eg. vitiligo, leucoderma, some
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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1; Mismatches
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                                                                                                                                                                                                                                                                                 (USSH ) US DEPT HEALTH & HUMAN SERVICES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 forms of albinism and hair greying
                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 26; Page 12; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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Job time: 63 secs
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Best Local Similarity
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Gaps

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Score 39; DB 4; Length 8; Pred. No. 1.4e+06; 0; Mismatches 1; Indels

Query Match 39.0%; Best Local Similarity 87.5%; Matches 7; Conservative (

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5, 2004, 10:56:07; Search time 66 Seconds (without alignments) 81.153 Million cell updates/sec
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2: /cgn2_6/ptodata/2/pubpaa/RCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/USOG_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/USOG_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/USOG_PUBCOMB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/USOG_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/USOG_PUBCOMB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/USOG_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/USOG_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/USOG_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USOG_PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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SUMMARIES	ID	US-09-761-636A-8	US-09-761-636A-27	US-09-761-636A-31	US-09-761-636A-2B	US-09-761-636A-30	US-09-761-636A-32	US-09-761-636A-29	US-09-761-636A-5	US-09-761-636A-15	US-09-761-636A-16	US-09-761-636A-18	US-09-761-6364-17	118-10-435-238-22	118-00-805-761-61	TO-TO/ COO CO CO	US-09-805-761-63
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16 US-10-600-187-78		-251-526-	-795-0		09-910-	12 US-10-362-527-115	12 US-10-362-527-156	9 US-09-779-308-461	US-10-43	US-09-784-553C	15 US-10-209-201C-58	10 US-09-932-613-67	10 US-09-932-322-67	-71	10 US-09-992-665-35	н	14 US-10-208-304-14	10 US-09-954-385-335	US-09-792-686A-1	13 US-10-139-841-9	US-10-014-485A	14 US-10-062-710-38	14 US-10-174-105A-9	9 US-09-829-549A-33	14 US-10-031-874A-158	US-09-226-157-	19-833-203-5	US-10-007-521-1	-10-007-521-
6	12	12	13	13	16	17	17	10	10	11	11	15	15	16	16	17	10	12	14	14	14	14	14	15	17	17	10	13	13
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16	17	18		20	21	22	23	24	25	26	27	28	59	30	31	32	33	34	35	36	37	86	39	40	41	42	43	44	45

ALIGNMENTS

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                                                                           APPLICANT: ACHEN, Marc

APPLICANT: ACHEN, Marc

APPLICANT: STACKER, Steven
APPLICANT: HUGHES, Richard
APPLICANT: CENDRON, Angela
ITILE OP INVENTION: USG-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
FILE REFERENCE: 1064/48505 Achen et al
CURRENT APPLICATION NUMBER: US 60/276,593
PRIOR FILING DATE: 2000-01-18
PRIOR FILING DATE: 2000-01-18
PRIOR PRILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PATENTIN VETSION 3.0
SEQ ID NOS BATCH IN VETSION 3.0
SEQ ID NOS BATCH IN VETSION 3.0
SEQ ID NOS BATCH IN VETSION 3.0
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100.0%; Pred. No. 3.2e-08;
1ve 0; Mismatches 0;
                     ; Sequence 8, Application US/09761636A; Patent No. US20020065218A1; GENERAL INFORMATION:
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Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
US-09-761-636A-8
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; Sequence 27, Application US/09761636A ; Patent No. US20020065218A1 RESULT 2 US-09-761-636A-27

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Gaps

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US-09-761-636A-30
; Sequence 30, Application US/09761636A
; Patent No. US20202065218A1
; Patent No. US20202065218A1
; GAPPLICANT: STACKEN, Marc
; APPLICANT: STACKEN, Steven
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT FILING DATE: 2001-01-18
; PRIOR PILING DATE: 2000-01-18
; PRIOR PILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFFWARE: PATENTIN VESTION 3.0
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Requence 32, Application US/09761636A

Retent No. US2002065218A1

GENERAL INFORMATION:

APPLICANT: ACHEN, Marc

APPLICANT: HUGHES, Richard

APPLICANT: APPLICATION WUMBER: US/09/761,636A

CURRENT FILING DATE: 2001-01-18

PRIOR APPLICATION NUMBER: US 60/176,293
TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 17;
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Pred. No. 3.7e-07;
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                     FILE REPERENCE: 1064/48505 Achen et al CURRENT APPLICATION NUMBER: US/09/761,636A CURRENT APLICATION NUMBER: US/09/761,636A CURRENT FILING DATE: 2001-01-18 PRIOR FILING DATE: 2000-01-18 PRIOR FILING DATE: 2000-01-16 NUMBER OF SEQ ID NOS: 34 SOFTWARE: Patentin version 3.0 SOFTWARE: Patentin version 3.0 LENGTH: 17
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88.2%;
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US-09-761-636A-30
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Best Local Similarity
Taches 15; Conservat
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LENGIH: 17
                                                                                                                                                                                                                                                                                        TYPE: PRT
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; Sequence 31, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
APPLICANT: STACKER, Steven
; APPLICANT: GENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF PEPTIDOMIMETIC INHIBITOR
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR PILING DATE: 2000-01-18
; PRIOR PILING DATE: 2000-05-16
                               APPLICANT: ACHEM. Marc
APPLICANT: STACKER, Steven
APPLICANT: STACKER, Steven
APPLICANT: STACKER, Steven
APPLICANT: CENDROW, Angela
TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
FILE REFREENCE: 1064/48505 Achen et al
CURRENT APPLICATION NUMBER: US 60/761,636A
CURRENT FILING DATE: 2001-01-189
PRIOR APPLICATION NUMBER: US 60/176,293
PRIOR PILING DATE: 2000-01-18
PRIOR PELING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PALENTIN VETSION 3.0
SEQ ID NO 27
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97.0%; Score 97; DB 9; Length 17;
Best Local Similarity 94.1%; Pred. No. 9.2e-08;
Matches 16; Conservative 1; Mismatches 0; Indels
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94.1%; Pred. No. 9.2e-08;
vative 1; Mismatches 0;
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Patent No. US20020065218A1
GENERAL INFORMATION:
APPLICANT: ACHEN, Marc
APPLICANT: STACKER, Steven
APPLICANT: HUGHES, Richard
APPLICANT: CENDRON, Angela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CASELGKSTNTYCKPPC 17
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SOFTWARE: Patentin version 3.0
SEQ ID NO 31
LENGTH: 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: synthetic construct
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Best Local Similarity 94.1
Matches 16; Conservative
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US-09-761-636A-31
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; TYPE: PRT; ORGANISM: synthetic construct US-09-761-636A-15
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Best Local Similarity 92.3
Matches 12; Conservative
             SEQ ID NO 5
LENGTH: 13
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                               US-09-761-636A-5
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Patent No. US2020065218A1

Recent No. US2020065218A1

APPLICANT: ACHEN, Marc

APPLICANT: STACKER, Steven

APPLICANT: CENDRON, Angela

TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR

FILE REFERENCE: 1064/48505 Achen et al

CURRENT APPLICATION NUMBER: US/09/761,636A

CURRENT FILING DATE: 2001-01-18

PRIOR APPLICATION NUMBER: US 60/176,293

PRIOR APPLICATION NUMBER: US 60/204,590

PRIOR PILING DATE: 2000-01-18

PRIOR FILING DATE: 2000-05-16

NUMBER OF SEQ ID NOS: 34

SOFTWARE: PATENTING VERSION 3.0
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FALCENT IN FUNCACUOSION.

FAPLICANT: ACHEN, MARC

APPLICANT: STACKER, Steven

APPLICANT: HUGHES, Richard

APPLICANT: CENTRON, Angela

TILE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR

FILE REFERENCE: 1064/48505 Achen et al

CURRENT APPLICATION NUMBER: US/09/761,636A

CURRENT PILING DATE: 2001-01-18

FRIOR APPLICATION NUMBER: US 60/176,293

PRIOR FILING DATE: 2000-01-18

FRIOR PELING DATE: 2000-05-16

NUMBER OF SEQ ID NOS: 34

SOFTWARE: PATENTIN VERSION 3.0
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PRIOR FILING DATE: 2000-01-18
PRIOR PEDLICATION NUMBER: US 60/204,590
PRIOR FILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 34
SEQ TWARE: Patentin version 3.0
LENGTH: 17
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; ORGANISM: synthetic construct
US-09-761-636A-32
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Best Local Similarity 82.4:
Matches 14; Conservative
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US-09-761-636A-29
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LENGTH: 17
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US-09-761-636A-16
Sequence 16, Application US/09761636A
Sequence 16, Application US/09761636A
Sequence 16, Application US/09761636A
Sequence 16, Application US/09761636A
GENERAL INCEMATION:
APPLICANT: APPLICANT: APCHEN, Marc
APPLICANT: CRUDON, Angela
TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
FILE REPERENCE: 1064/48505 Achen et al
CURRENT APPLICATION NUMBER: US/09/761,636A
CURRENT FILING DATE: 2000-01-01-18
PRIOR FILING DATE: 2000-01-01-18
PRIOR FILING DATE: 2000-01-16
PRIOR FILING DATE: 2000-05-16
NUMBER: OF SEQ ID NOS: 34
SOFTWARE: PatentIn version 3.0
SEQ ID NO 16
LENGTH: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 9
US-09-761-636A-15
i Sequence 15. Application US/09761636A
j Patent No. US20020065218A1
j GENERAL INFORMATION:
i APPLICANT: STACKER, Steven
j APPLICANT: STACKER, Steven
j APPLICANT: BTACKER, Steven
j APPLICANT: HUGHES, Richard
j TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
j TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF
j TILLE OF INVENTION: VEGF-D/VEGF-C/VEGF
j CURRENT APPLICATION NUMBER: US/09/761,636A
j CURRENT FILING DATE: 2001-01-18
pRIOR PLILING DATE: 2000-01-18
pRIOR PLILING DATE: 2000-01-18
pRIOR PLILING DATE: 2000-01-18
j PRIOR PLILING DATE: 2000-01-18
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j RIOR PLILING DA
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                                            Length 13;
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DB 9; Leas.
                   Query Match 72.0%; Score 72; DB Best Local Similarity 100.0%; Pred. No. 0.( Matches 13; Conservative 0; Mismatches
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                                                                                                                                                                                               Sequence 22, Application US/10435238
| Publication No. US20030224972A1
| GENERAL INFORMATION:
| APPLICANT: HEARING, Vincent J., Jr. |
| TITLE OF INVENTION: Depigmenting Activity of Agouti Signal |
| Protein and Peptides Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37.0%; Score 37; DB 12; Length 10; 66.7%; Pred. No. 64; 2; Indels tive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 14

US-09-805-761-61

Squence 61, Application US/09805761

Patent No. US20020165174A1

GENERAL INFORMATION:

APPLICANT: Gill, Parkesh

APPLICANT: Mascod, Rizwan

TITLE OF INVENITON: WETHOOS AND COMPOSITIONS FOR ANTISENSE

TITLE OF INVENITON: VEST OLIGONUCLEOTIDES

FILE REFERENCE: 21327-701CON2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 30303-1811
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/435,238
FILING DATE: 08-May-2003
CLASSIFICATION: <unburelens of the control of the contr
                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Needle & Rosenberg, P.C.
STREET: 127 Peachtree St., N.E.
CITY: Allanta
STATE: GA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (404) 688-9880
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 10 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 66...
6, Conservative
                 1 CASDVGKSTNTWC 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ATNDSCKPP 9
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                                                                                                                                               RESULT 13
US-10-435-238-22
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                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                               Sequence 18, Application US/09761636A
; Sequence 18, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
    APPLICANT: ACHEN, Marc
    APPLICANT: CRUNEWN
    APPLICANT: HUGHES, Richard
    APPLICANT: HUGHES, Richard
    APPLICANT: HUGHES, Richard
    APPLICANT: HUGHES, Richard
    TITLE OF INVENTION: VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
    TILE REFERENCE: 1064/48505 Achen et al
    CURRENT APPLICATION: VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
    FILE REFERENCE: 1064/48505 Achen et al
    CURRENT FILING DATE: 2000-10-18
    PRIOR FILING DATE: 2000-01-18
    PRIOR FILING DATE: 2000-05-16
    NUMBER OF SEQ ID NOS: 34
    SOFTWARE: PatentIn version 3.0
    SEQ ID NO 18
    LENGTH: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 17, Application US/09761636A
; Sequence 17, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
    APPLICANT: ACHEN, Marc
    APPLICANT: STACKER, Steven
    APPLICANT: CENDROM, Angela
    TITLE OF INVENTION VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
    TITLE OF INVENTION VEGF-D/VEGF-C/VEGF
    TILE REFERENCE: 1064/4856 Achen et al
    CURRENT APPLICATION NUMBER: US/09/761,636A
    CURRENT PILING DATE: 2000-01-18
    PRIOR FILING DATE: 2000-01-18
    PRIOR FILING DATE: 2000-01-18
    PRIOR FILING DATE: 2000-01-18
    NUMBER OF SEQ ID NOS: 34
    SOFTHARE: PATENTIN VERSION 3.0
    SOFTHARE: PATENTIN VERSION 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65.0%; Score 65; DB 9; Length 13; 84.6%; Pred. No. 0.0049; tive 2; Mismatches 0; Indels
                       Length 13;
                                                                                        0; Indels
                    Score 65; DB 9;
Pred. No. 0.0049;
2; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
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US-09-761-636A-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , OKGANISM: SYNthetic construct
US-09-761-636A-18
                              65.0%;
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Query Match
Best Local Similarity 84.0.
Best Local 11, Conservative
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                                                                                                                                                                                                      1 CASELGKTSNTFC 13
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JOSTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 32.0%; Score 32; DB 9; Length 7; Best Local Similarity 85.7%; Pred. No. 1.2e+06; Matches 6; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32.0%; Score 32; DB 9; Length 7; 85.7%; Pred. No. 1.2e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                             CORRENT AFTLANGO NUMBER: US/09/805,761
CORRENT FILING DATE: 2001-03-13
PRIOR APPLICATION NUMBER: PCT/USO1/00019
PRIOR PILING DATE: 2001-01-19
PRIOR PLING DATE: 2000-01-19
PRIOR FILING DATE: 2000-01-19
PRIOR FILING DATE: 2000-11-24
PRIOR FILING DATE: 2000-11-24
PRIOR PLING DATE: 1998-01-30
PRIOR PLING DATE: 1998-01-30
PRIOR PLING DATE: 1998-01-30
PRIOR PLING DATE: 1997-01-31
NUMBER OF SEQ ID NOS: 64
SOFTWARE: FREUER FORESTER OF SEQ ID NOS: 64
SEQ ID NO 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
CURRENT APPLICATION NUMBER: US/09/805,761
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Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Homo sapiens
US-09-805-761-61
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; ORGANISM: Homo sapiens
US-09-805-761-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 INTECKP 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |||| ||
1 TNTFFKP 7
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GenCore version 5.1.6
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OM protein - protein search, using sw model

5, 2004, 10:53:36; Search time 20 Seconds (without alignments) 43.882 Million cell updates/sec September Run on:

US-09-761-636A-8

100 1 CASELGKSTNTFCKPPC 17 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

389414 segs, 51625971 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 17

Post-processing: Minimum Match 0* Maximum Match 100* Listing first 45 summaries

Issued Patents AA:*

: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*

: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*

: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*

: /cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*

: /cgn2_6/ptodata/2/iaa/PcTuS_COMB.pep:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description		, c	Sequence 76, Appl		ן ר	7 4	r -	Segmence 21 Appli	4	. 4	·σ	٠,	ì	10	Semionce 9, Applia	,	٠,	7 <	Semience 1, Appril		000	000	, 1	,	102		102.	104,
SUMMARIES	ID	US-08-983-1578-22	-09-644-600-7	-09-654-	-08-053-079A-	3-685-589A-	-09-462-118-4	-08-369-566-	-08-983-	US-09-328-501-4	-60-	US-08-882-046-9	US-09-252-586-19		-08-425-989B-	-08-443-966B-	-853-910-3	-09-148-712-	-08-487-485A-	US-08-400-115-26	08-637-759	08-871-355A-40	-201-945-	C 3CT10-303	1-1367-1	1-0001-100-00	-08-51-136C-1	-09-229-911A-10	US-09-229-911A-104
	Length DB	10 4	9	9	12 1	12 2	12 4	16 1	10 4	16 3	16 4	17 3	17 4	14 2	14 2	14 2	14 3	14 4	15 1	17 2	10 2	10 3	10 4	_	3 5			T :	13 4
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	Score	37	32	32	32	32		32	31	31	31	31	31	30	30	30	30	30	29.5	9	29	29	29	53	29	29	000	9 0	73
	Result No.	н	7	m	4	2	9	7	ω (, D (10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26		

Sequence 23, Appl Sequence 12, Appl Sequence 24, Appl Sequence 24, Appl Sequence 63, Appl Sequence 63, Appl Sequence 61, Appl Sequence 11, Appl Sequence 12, Appl Sequence 16, Appl Sequence 11,	sequence 41, Appl
US-08-182-967-23 US-07-689-693B-12 US-09-230-222-3 US-09-280-722-24 US-09-09-286-754-63 US-09-042-107-63 US-09-142-107-63 US-09-111-681C-8 US-09-111-681C-8 US-09-111-681C-13 US-09-111-681C-16 US-09-111-681C-16 US-09-114-81C-16 US-09-141-18-10-16 US-09-141-18-10-16 US-08-141-18-25A-19 US-08-141-18-25A-19 US-08-141-18-25A-11 US-08-141-18-25A-11 US-08-141-18-25A-11	18-W/88-505-55-55
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ALIGNMENTS

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APPLICANT: HEARING, Vincent J., Jr.
TITLE OF INVENTION: Depigmenting Activity of Agouti Signal
Protein and Peptides Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/983,157B
FILING DATE: 22-Dec-1997
CLASSIFCATION DATA:

APPLICATION NUMBER: DCT/US96/10695
FILING DATE: 21 JUN 1996
APPLICATION NUMBER: PCT/US96/10695
ATORNEY/AGENT INFORMATION:

NAME: Spratt, Gwendolyn D.

REGISTRATION NUMBER: 36,016

REGISTRATION NUMBER: 36,016

REGISTRATION NUMBER: 36,016

REGISTRATION NUMBER: 36,016
                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSE: Needle & Rosenberg, P.C.
STREET: 127 Peachtree St., N.E.
CITY: Atlanta
STATE: GA
                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 30303-1811
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-08-983-1578-22
                      Sequence 22, Application US/08983157B
Patent No. 6579848
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 688-0770
TELEFAX: (404) 688-9880
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 10 amino acids
TYPE: amino acid
                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
US-08-983-157B-22
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Gaps

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Query Match
37.0%; Score 37; DB 4; Length 10;
Best Local Similarity 66.7%; Pred. No. 15;
Matches 6; Conservative 1; Mismatches 2; Indels

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STRANDEDNESS:
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US-08-685-589A-228
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               US-08-053-079A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
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                                                                                                                                                                                                     Sequence 78, Application US/09644600

Sequence 78, Application US/09644600

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
TITLE OF INVENTION: TADO-15: AD Extracellular Serine Protease:
TITLE OF INVENTION NUMBER: US/09/644,600

CURRENT FILING DATE: 1998-10-20

PRIOR FILING DATE: 1998-10-20

PRIOR FILING DATE: 1998-02-20

NUMBER OF SEQ ID NOS: 98

SEQ ID NO 78

INVENTIOR PRIOR PRI
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Sequence 70.8.

Sequence 70.8.

Sequence 70.8.

Patent No. 664974.

GENERAL INFORMATION:

APPLICANT: O'BITACH.

TITLE OF INVENTION: O'VERENCESSEG in Carcinomas

FILE REFERENCE: D606410P/D

CURRENT APPLICATION NUMBER: US/09/654,600A

CURRENT FILING DATE: 1909-10-20

PRIOR FILING DATE: 1999-10-20

1998-02-20

NUMBER OF SEQ ID NOS: 98

SEQ ID NO 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Residues 495-503 of the TADG-15 protein US-09-644-600-78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 32; DB 4; Length 9;
Pred. No. 3e+05;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
32.0%; Score 32; DB 4; Length 9;
Best Local Similarity 83.3%; Pred. No. 3e+05;
Matches 5; Conservative 0; Mismatches 1; Indels
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83.3%;
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Best Local Similarity 83.3
Matches 5; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
8 STNTFCKPP 16
                                               10 NTFCKP 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Chang, Conway
APPLICANT: Chang, Leo
APPLICANT: Chen, Jie
TITLE OF INVENTION: CYCLIC PEPTIDES HAVING BROAD
TITLE OF INVENTION: SPECTRUM ANTIMICROBIAL ACTIVITY
NUMBER OF SEQUENCES: 222
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
Sequence 4, Application US/08053079A; Sequent No. 5606026; Bareal INFORMATION:
APPLICANT: ROGMAN
TITLE OF INTENTION: Natural Human IgM Antibodies
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby
STREET: 805 Third Ave.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Human immunodeficiency virus type 1
IMMEDIATE SOURCE:
CLONE: tat #4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Robinson, Joseph, R.
REGISTRATION NUMBER: 33,448
REFERENCE/DOCKET NUMBER: 4436/16060US4
RELECOMMUNICATION INFORMATION:
TELECOMMUNICATION: (212)527-7700
TELEPHONE: (212)537-7700
                                                                                                                                                                                                                                                                  COUNTIES CONTROLL OF THE CONTROLL OF THE COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: BW PC COMPATIBLE
COMPUTER: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/053,079A
FILLING DATE: 26-APR-1993
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 228, Application US/08685589A
; Patent No. 5916872
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 236687
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32.0
Best Local Similarity 55.6
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide HYPOTHETICAL: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
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                                                                                                                                                                                                                                    New York
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APPLICANT: Bausher, Michael G
TITLE OF INVENTION: Citrus Proteins for Use in Field
TITLE OF INVENTION: Detection of Citrus Blight Using Immunological Techniques NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSE: USDA-ARS
STREET: Room 408, Bldg 005, BARC-W
CITY: Beltsville
STATE: Maryland
COUNTRY: USA
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Sequence 21, Application US/08983157B
Patent No. 6579848
GENERAL INFORMATION:
APPLICANT: HEARING, Vincent J., Jr.
TITLE OF INVENTION: Depigmenting Activity of Agouti Signal
Protein and Peptides Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32.0%; Score 32; DB 1; Length 16; 54.5%; Pred. No. 1.46+02; live 1; Mismatches 4; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/369,566
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ADDRESSEE: Needle & Rosenberg, P.C. STREET: 127 Peachtree St., N.E. CITY: Atlanta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/792,508
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US/08/369,566
                                                                                                              Sequence 1, Application US/08369566; Patent No. 5650151; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 20705
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 301-344-1003
TELEFAX: 301-344-5060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 301-344-5060
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32.0
Best Local Similarity 54.5
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 GKSTNTFCKPP 16
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                2 TNCYCKKCC 10
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                                                                                               US-08-369-566-1
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MAME/KEY: Modified-site
LOCATION: 12
OTHER INFORMATION: /product= "Xaa=Cha=cyclohexylalanine"
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Patent No. 6610833
GENERAL INFORMATION:
APPLICANT: ROGMEN, Toby C.
TITLE OF INVENTION: Monoclonal Human Natural Antibodies
CURRENT APPLICATION NUMBER: US/09/462,118
CURRENT FILING DATE: 1999-12-18
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSEQ for Windows Version 3.0
                                                  COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/685,589A
FILING DATE: 24-UUL-1996
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 32; DB 2;
Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                    NAME: COTUZZI, LAUTA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8067-026-999
TELECOMUNICATION INFORMATION:
TELEPHONE: 212-790-9990
TELEPAX: 212-869-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: 1..12
OTHER INFORMATION: /product= "Cyclic"
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                                                                                                                                                                                             FILING DATE: 24-UU-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
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83.3%;
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TELEX: 66141
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
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MOLECULE TYPE: peptide
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  New York
: USA
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Matches 5: Conserv
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Best Local Similarity
Matches 5; Conserv
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                                         10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-685-589A-228
STATE: N
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Pred. No. 2.1e+02;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                    Length 16;
                                                                                                                                                                                                                                                                                                                                                                              Score 31; DB 4; Length 16;
Pred. No. 1.9e+02;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 9, Application US/08882046

| Sequence 9, Application US/08882046
| Patent No. 6136952
| GENERAL INFORMATION:
| APPLICANT: Li, Linheng APPLICANT: Hood, Leroy
| APPLICANT: Krantz, Ian D. APPLICANT: Spinner, Nancy B. TITLE OF INVENTION: Human Jagged Polypeptide, Encoding TITLE OF INVENTION: Nucleic Acids and Methods of Use NUMBER OF SEQUENCES: 110
| CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER KALLABLE FORD

COMPUTER: Floppy disk

COMPUTER: IBM PC Compatible

COMPUTER: IBM PC Compatible

COMPUTER: IBM PC Compatible

COMPUTER: Patentin Release #1.0, Version #1.25

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION NUMBER: US/08/882,046

FILING DAYE: 25-JUN-1997

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815

REGISTRATION NUMBER: 31,815

REGISTRATION NUMBER: 9-UW 2637

TELEFONNICATION INFORMATION:

TELEFONE: (619) 535-9001

TELEFONE: (619) 535-8949

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Campbell & Flores LLP
4370 La Jolla Village Drive, Suite 700
TITLE OF INVENTION: CERAMIDASE GENE
FILE REFERENCE: 1422-0458P
CURRENT APPLICATION NUMBER: US/09/777,710A
CURRENT FILING DATE: 201-02-07
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin version 3.0
SEQ ID NO 4
                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31.0%;
50.0%;
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60.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 60.0
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | | | ||:|
7 GFGCNKFCRP 16
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2 SEIGGSTRSF 11
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STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
3Y: linear
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Best Local Similarity
Matches 5; Conserv
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STREET: 43'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 92122
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US-08-882-046-9
                                                                                                                                                                                                                                      LENGTH: 16
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Pred. No. 1.9e+02;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 31.0%; Score 31; DB 4; Length 10; Best Local Similarity 55.6%; Pred. No. 1.2e+02; Matches 5; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                             NAME: Spratt, Gwendolyn D.
REGISTRATION NUMBER: 36,016
REGISTRATION NUMBER: 36,016
REFERENCE/DOCKET NUMBER: 14014.0195
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 688-9880
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
FENGUENCE CHARACTERISTICS:
FENG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/09328501A; Sequence 4, Application US/09328501A; Patent No. 625681

GENERAL INFORMATION:
APPLICANT: OKINO, No. 62585810mu; APPLICANT: ITO, Makoto
TITLE OF INVENTION: Ceramidase Gene; FILE REFERENCE: 1422-0377P; CURRENT APPLICATION UNMBER: US/09/328,501A; CURRENT APPLICATION NUMBER: 10-234769 JAPAN EARLIER PILING DATE: 1999-06-09; MUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 4
LENOTH: 16
                                                   PRIOR APPLICATION NUMBER: US/08/983,157B
FILING DATE: 22-Dec-1997
CLASSIFICATION: «Unknown»
PRIOR APPLICATION NUMBER: PCT/US96/10695
FILING DATE: 21 JUN 1996
APPLICATION NUMBER: 60/000,436
FILING DATE: 23 JUN 1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: any n or Xaa = Unknown US-09-328-501-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: not relevant
STRANDEDNESS: not relevant
TOPOLOGY: linear
SEQUENCE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-08-983-1578-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/09777710A
Patent No. 6489117
GENERAL INFORMATION:
APPLICANT: OKINO, No. 64891170mu et al.
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                             CURRENT APPLICATION DATA:
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Best Local Similarity 60.v
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SEIGGSTRSF 11
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US-09-777-710A-4
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US-09-328-501-4
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Gaps
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residues correspond to the C-terminus of
ICAM; last residue (Cys) added to faciliate
coupling
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Patent No. 5845699
GENERALI INFORMATION:
APPLICANT: McClelland, Alan
APPLICANT: Greve, Jeffrey M.
TITLE OF INVENTION: Soluble Molecule Related to but
TITLE OF SEQUENCES: 13
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" diskette, 1.44 MB storage
COMPUTER: IBM ThinkPad 760ED
                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 08/156,653
FILING DATE: 22-NOV-1993
FILING DATE: 22-NOV-1993
FILING DATE: 15-JAN-1993
APPLICATION NUMBER: 07/449,356
FILING DATE: 10-DEC-1989
APPLICATION NUMBER: 07/445,951
FILING DATE: 13-DEC-1989
APPLICATION NUMBER: 07/301,192
FILING DATE: 24-JAN-1989
APPLICATION NUMBER: 07/301,192
FILING DATE: 07/445,951
FILING DATE: 07/449,951
FILING DATE: 07/449,91
FILING DA
                                                 OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/443,965B
FILING DATE: 18-MAY-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: modified ICAM fragment
JOCATION: C-terminus
CTHER INFORMATION: first 11 amino
OTHER INFORMATION: residues corre
OTHER INFORMATION: ICAM; last res
GTHER INFORMATION: coupling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C-terminal fragment
                                                                                                                                                                                                                                      08/425,989
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                            IBM ThinkPad 760ED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bayer Corporation
                                                                                                                                                                                                                                   APPLICATION NUMBER: 08/42
FILING DATE: 20-APR-1995
APPLICATION NUMBER: 08/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: BAYER CORPORATE STREET: 400 Morgan Lane CITY: West Haven STATE: Connecticut COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
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US-08-425-989B-9
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                                                    Sequence 19, Application US/09252586
Patent No. 6387643
GENERAL INFORMATION:
APPLICANT: Heinrikson, Robert L.
APPLICANT: Fairbanks, Michael B.
APPLICANT: Midner, Ana M.
TITLE OF INVENTION: Human Platelet Heparanase Polypeptides,
TITLE OF INVENTION: Polynucleotide Molecules That Encode Them, and Methods For ITLE OF INVENTION: Activity
NUMBER OF SEQUENCES: 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: McClelland, Alan
APPLICANT: Greve, Jeffrey M.
TITLE OF INVENTION: Soluble Molecule Related to but
TITLE OF INVENTION: Distinct from ICAM-1
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, Version #1.25 APPLICATION DATA:
APPLICATION NUMBER: US/09/252,586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 06516
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" diskette, 1.44 MB storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6131.N CN1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Kerber, Lori L.
REGISTRATION NUMBER: 41,113
REFERENCE/DOCKET NUMBER: 6131.
TELEPHONE: 616-833-0974
TELEFAX: 616-833-0974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9, Application US/08443965B Patent No. 5821341
                                                                                                                                                                                                                                                                                                                                                                                                                           E: Pharmacia & Upjohn
301 Henrietta
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STREET: 400 Morgan Lane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 49001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 ELGKSTNTFCK 14
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CITY: West Haven
STATE: Connecticut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
DGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Kalamazoo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                        US-09-252-586-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
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RESULT 12
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Search completed: September 5, 2004, 10:56:57
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TOPOLOGY:
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NAME/KEY: modified ICAM fragment
LOCATION: C-terminus
OTHER INFORMATION: first 11 amino acid
OTHER INFORMATION: residues correspond to the C-terminus of
OTHER INFORMATION: CAM; last residue (Cys) added to faciliate
OTHER INFORMATION: coupling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | Sequence 9, Application US/08443966B | Sequence 9, Application US/08443966B | Patent No. 585912 | Seminary McClelland, Alan APPLICANT: McClelland, Alan APPLICANT: Gree, Jeffrey M. TITLE OF INVENTION: Soluble Molecule Related to but TITLE OF INVENTION: Distinct from ICAM-1 | STREET: 400 Morgan Lane | STREET: 400 Morgan Lane | STREET: West Haven | STREET: COUNTRY: USA | COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA

ZIP: 06516
COMPUTER READBLE FORM:
COMPUTER: 3.5" diskette, 1.44 MB storage
COMPUTER: 1BM ThinkPad 760ED
COMPUTER: Wardows 95
COFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/425,989B
FILING DATE: 20-APR-1995
PRIOR APPLICATION NUMBER: 08/156,653
FILING DATE: 22-NOV-1993
APPLICATION NUMBER: 08/105,204
FILING DATE: 15-JAN-1993
APPLICATION NUMBER: 07/449,356
FILING DATE: 21-DEC-1989
APPLICATION NUMBER: 07/449,366
FILING DATE: 13-DEC-1989
APPLICATION NUMBER: 07/301,192
FILING DATE: 24-JAN-1989
APPLICATION NUMBER: 07/301,192
FILING DATE: 3-JAN-1989
APPLICATION NUMBER: 07/301,192
FILING DATE: 3-JAN-1989
APPLICATION NUMBER: 07/301,192
FILING DATE: 24-JAN-1989
APPLICATION NUMBER: 07/301,192
FILING DATE: 24-JAN-1989
APPLICATION NUMBER: 07/301,192
FILING DATE: 21-SAN-1989
APPLICATION NUMBER: 07/301,192
FILING DATE: 2786
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION NUMBER: 07/301,192
TELEFARM: (203) 812-2786
TELEFARM: 07/301,103
FENDENCE CHRRACTERISTICS: 07/301,103
FENDENCE CHRRACTERISTICS: 07/301,103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYPOTHETICAL: no FRAGMENT TYPE: C-terminal fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 14 amino acid residues
TYPE: amino acid
TOPOLOGY: linear
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DESCRIPTION: peptide
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Gaps
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CTHER INFORMATION: first 11 amino acid
CTHER INFORMATION: residues correspond to the C-terminus of
CTHER INFORMATION: ICAM; last residue (Cys) added to faciliate
COTHER INFORMATION: coupling
US-08-443-966B-9
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APPLICATION NUMBER: US/08/443,966B
FILING DATE: 18-MAY-1995
APPLICATION NUMBER: 08/425,989
FILING DATE: 20-APR-1995
APPLICATION NUMBER: 08/156,653
FILING DATE: 20-MOV-1993
APPLICATION NUMBER: 08/105,204
FILING DATE: 15-JAN-1993
APPLICATION NUMBER: 07/449,356
FILING DATE: 12-DEC-1989
APPLICATION NUMBER: 07/445,951
FILING DATE: 13-DEC-1989
APPLICATION NUMBER: 07/445,951
FILING DATE: 13-DEC-1989
APPLICATION NUMBER: 07/445,951
FILING DATE: 24-MA-1989
ATTOMEY/ABRIT INFORMATION:
NAME: BATBERT INFORMATION:
TELEPHONE: (203) 812-2786
TELEPROMICATION INFORMATION:
TELEPHONE: (203) 812-2786
TELEPROMICATION INFORMATION:
TELEPHONE: (203) 812-2786
TELEPROMICATION INFORMATION:
TELEPHONE: (203) 812-2786
TELEPHONE: (203) 812-5786
TELEPROMICATION INFORMATION:
TELEPHONE: (203) 812-5786
TELEPROMICATION INFORMATION:
TELEPHONE: (203) 812-5786
TELEPROMICATION FOR SEQ ID NO: 9:
REQUINCE CHARRACTERISTICS:
TANDEL AMILIA AMILIA ACIÓN TESIGIQUES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C-terminal fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: modified ICAM fragment
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Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
DESCRIPTION: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 NTFCKPPC 17
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GY: linear
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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protein search, using sw model OM protein -

5, 2004, 11:00:28; Search time 11.6667 Seconds (without alignments)
74.205 Million cell updates/sec September Run on:

Title: Perfect score:

US-09-761-636A-9 55 1 CCNEESLIC 9 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283366 seqs, 96191526 residues Searched:

790 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 9 Minimum DB (Maximum DB (

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

fibrinogen beta ch leucine-tRNA ligas hypothetical TCL3 fibrinogen beta ch T-cell receptor be jacalin beta-II ch T protein - human T-cell receptor be fibrinopeptide B -fibrinopeptide B -fibrinopeptide B -fibrinopeptide B -Tibrinopeptide B -Tibrinopeptide B -Tibrinopeptide B -Tibrinopeptide B -Tibrinopeptide B -T-cell receptor be ferredoxin a2. Ja transaldolase (BC cardioactive pepti cardioactive pepti T-cell receptor be cardioactive pepti dibydrofolate redu lipopeptide WS1279 calsequestrin, fas metallothionein is acylase - Kluyvera aspartate kinase (calsequestrin, car octamer-binding pr Na+/K+-exchanging galactose oxidase Description SUMMARIES PC1002 179564 D24180 PH0942 S29637 I37263 PH0932 D28854 E28854 F28854 PH0935 PH0921 JU0355 B39040 S59622 S19288 S69165 A11497 A26363 S27233 \$39767 B31263 \$29881 XEYDGD B47594 A61230 B39504 C24180 H DB Length Query Match Score Result No.

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T-cell receptor be	traM protein - Esc	snerm-activative	Sprim amyloid D-oo	Id heavy chain con	Tropl recent by	TOUGHT TECCED TO	Z-cert receptor De	917copiocem compo	FORMAL SINCE	proximy 1917 Ciliamine	⊣`	protoin n n-1	mironia inhibiti	**************************************	The little of the state of the
7	5 2 A32014 8 2 A37521	N	7	9 2 PT0272	9 2 PH0943	9 2 PH0902	6 2 H48394		7 2 A12016					5 2 B22565	
14 25.5	13 23.6		13 23.6	13 23.6	13 23.6	13 23.6		12 21.8					11 20.0		
30	35	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

EESULT 1 C24180 Librinogen beta chain - Japanese macaque (fragment) N.Contains: Tibrinopeptide B C.Species: Macaca fucata (Japanese macaque) A.Faciente. 97, 1487-1492, 1985 A.Fille: Pibrinopeptides A and B of Japanese monkey (Macaca fuscata) and patas monkey (E A.Reference mumber: A91990; MUID:85289140; PMID:3928610 A.Faciente. 19. AMACA C.Superfamily: fibrinopen beta chain; fibrinogen beta/gamma homology; fibrinogen disulf; C.Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulf; C.Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulf; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0; M.Alternate names: Leucyl-trNA synthetase D. N.Alternate names: Leucyl-trNA synthetase C.Species: Recheiding coli C.Species: Re	Query Match 34.5%; Score 19; DB 2; Length 8; Best Local Similarity 66.7%; Pred. No. 2.8e+05; Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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Section beta-II chain - Artocarpus champeden (fragment)
C;Species: Artocarpus champeden
C;Date: 19-Mar-1997 #sequence_revision 24-Jul-1998 #text_change 24-Jul-1998
C;Date: 19-Mar-1997 #sequence_revision 24-Jul-1998 #text_change 24-Jul-1998
C;Date: 19-Mar-1997 #sequence_revision 24-Jul-1998 #text_change 24-Jul-1998
C;Accession: 829637
B;Ngoc, L.D.; Brillard, M.; Hoebeke, J.
B;Ochim. Biophys. Acta 1156, 219-222, 1993
A;Title: The alpha- and beta-subunits of the jacalins are cleavage products from a 17-kD.
A;Reference number: 829635; MUID:93152601; PMID:8427879
A;Accession: 829637
A;Molecule type: protein
A;Residues: 1-6 <NGO>
A;Experimental source: seed
C;Complex: heterotetramer; two alpha and two beta chains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           137263
Y protein - human (fragment)
Y protein - human (fragment)
C;Species: How sapiens (man)
A;Reference humber: How sapiens (man)
A;Reference number: How sapiens (man)
A;Reference number: How sapiens (man)
A;Reference humber: How sapiens (man)
A;Reference humber:
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C;Gecies: Rattus norvegicus (Norway rat)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C;Accession: PH0932
C;Accession: PH0932
J Exp. Med. 174, 1467-1476, 1991
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allery
A;Reference number: PH0891; MUID:92078857; PMID:1836012
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A;Cross-references: EMBL:X68994; NID:g396171; PIDN:CAA48780.1; PID:g579816
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A;Note: lectin for D-galactosyl-beta-1->3-N-acetylgalactosamine
C;Keywords: heterotetramer; lectin; seed; storage protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
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75.0%; Pred. No. 2.8e+05;
Live 0; Mismatches 1; Inde
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 17; DB 2; Length
Pred. No. 2.8e+05;
1; Mismatches 0; Inde
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 30.9%;
Best Local Similarity 75.0%;
Matches 3; Conservative
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Best Local Similarity 75..
Best Local 3; Conservative
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    N
1 CC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 8
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            à
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J. Exp. Med. 174, 1467-1476, 1991
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergial Reference number: PH0891; MUID:92078857; PMID:1836012
A;Accession: PH0942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                uenons, and baboons.
A;Reference number: A91990; MUID:85289140; PMID:3928610
A;Accession: D24180
A;Accession: protein
A;Residues: 1-9 <NAK>
C;Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfi
                                                                                                                             C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 28-Jan-2000 #sequence_revision 28-Jan-2000 #text_change 28-Jan-2000
C;Date: 28-Jan-2000 #sequence_revision 28-Jan-2000 #text_change 28-Jan-2000
C;Accession: 179564
R;Zutter, M.; Hockett, R.D.; Roberts, C.W.; McGuire, E.A.; Bloomstone, J.; Morton, C.C.; Proc. Natl. Acad. Sci. U.S.A. 87, 3161-3165, 1990
A;Title: The t(10;14) (q24;q11) of T-cell acute lymphoblastic leukemia juxtaposes the del A;Teference number: 159162; MUID:9022189; PMID:2326274
A;Accession: 179564
A;Status: translation not shown; translated from GB/EMBL/DDBJ
A;Molecule: type: DNA
A;Molecule: 16 <2UT>
A;Colment: This is the hypothetical translation of a sequence translated in an incorrect
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N;Contains: fibrinopeptide B
C;Species: Brythrocebus patas (red guenon, hussar)
C;Species: Brythrocebus patas (red guenon, hussar)
C;Date: 05-Jun-1988 #sequence_revision 10-Mar-1994 #text_change 26-Jan-1996
C;Datession: D4180
C;Macamura, S:; Takenaka, O:; Takahashi, K.
J; Blochem. 97, 1487-1492, 1985
A;Title: Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and patas monkey
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C;Accession: PH0942
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A;Residues: 1-9 <GOL>
A;Resimental source: complete Freund's adjuvant-immunized lymph node
A;Rotes: the authors translated the codon TGC for residue 2 as Ala
C;Keywords: T-cell receptor
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                                                                                            hypothetical ICL3 protein (mistranslated) - human (fragment)
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Best Local Similarity
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A;Molecule type: protein
A;Residues: 1-9 <NAK>
C:Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfi
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R,Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
R,Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
A,Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergi
A,Reference number: PH0891; MUID:92078857; PMID:1836012
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C;Species: Rattus norvegicus (Norway rat)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997

C;Accession: PH0921

R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.

J. Exp. Med. 174, 1467-1476, 1991

A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allerging the process of the process o
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R;Tsuda, Y.; Okada, Y.; Tanaka, M.; Shigematsu, N.; Hori, Y.; Goto, T.; Hashimoto, M. Chem. Pharm. Bull. 39, 607-611, 1991
A;Title: Structure and synthesis of an immunoactive lipopeptide, WS1279, of microbial or A;Reference number: JU0355; MUID:91300586; PMID:2070441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T-cell receptor beta chain V-D-J region (clone 6) - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 09-0ct-1992 #sequence_revision 09-0ct-1992 #text_change 30-May-1997
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C;Species: Streptomyces willmorei
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
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30.9%; Score 17; DB 2; Length 9;
Best Local Similarity 60.0%; Pred. No. 2.88+05;
Matches 3; Conservative 1; Mismatches 1; Indels
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2; Mismatches 2; Indels
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Best Local Similarity 33.3%;
-hes 2; Conservative
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Best Local Similarity 33.5%,
2, Conservative
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A; Residues: 1-9 <GOL>
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A; Residues: 1-9 <GOL>
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C;Species: Papio anubis, Papio hamadryas anubis (olive baboon)
C;Species: Papio anubis, Papio hamadryas anubis (olive baboon)
C;Accession: D28894
B;Nacamura, S.; Takenaka, O.; Takahashi, K.
J. Biochem. 94, 1973-1978, 1983
A;Title: Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas, and Theropit
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A;Residues: 1-9 <NAK>
C;Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfi
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R;Nakamura, S.; Takenaka, O.; Takahashi, K.
J. Biochem. 94, 1973-1978, 1983
A;Title: Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas, and Theropit A;Reference number: A91973; MUID:84161822; PMID:6423621
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A;Residues: 1-9 <NAK>
C:Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfi
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C.Species: Theropithecus gelada (gelada baboon)
C.Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 18-Aug-2000
C.Accession: F28854
B;Nakamura, S.; Takenaka, O.; Takahashi, K.
B;Nakamura, I 1973-1978, 1983
A;Title: Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas, and Theropit
A;Reference number: A91973; MUID:84161822; PMID:6423621
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C:Species: Papio hamadryas (hamadryas baboon)
C:Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 18-Aug-2000
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A;Molecule type: mRNA
A;Residues: 1-7 <GOL>
A;Experimental source: complete Freund's adjuvant-immunized lymph node
C;Keywords: T-cell receptor
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Pred. No. 2.8e+05;
1; Mismatches 3; Indels
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Matches 3: Conserv
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Best Local Similarity
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Matches 3; Conserv
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A;Accession: JU0155
A;Molecule type: protein
A;Residues: 1-6 <TSU>
A;Note: the structure was confirmed by synthesis
C;Keywords: blocked amino end; lipoprotein
F;I/Binding site: sn-2,3-diacylglycerol (Cys) (covalent) #status experimental
F;I/Modified site: fatty acylated amino end (Cys) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                  Gaps
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                                                                                                     Query Match

27.3%; Score 15; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match

27.3%; Score 15; DB 2; L
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 1;
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Search completed: September 5, 2004, 11:06:22 Job time: 12.6667 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

5, 2004, 10:57:02; Search time 7 Seconds (without alignments) 66.947 Million cell updates/sec September Run on:

US-09-761-636A-9 55 1 CCNEESLIC 9 Title: Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Sequence:

251 141681 seqs, 52070155 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	P19345 macaca fusc	46 erythro	4	43	2 therop	31	99	P17441 pichia jadi	4 dactyli	m	_	P19095 mustelus ca	_	P30087 homo sapien	7 Btomo	_	conus i	ascari	_	P82926 bos taurus	P30093 homo sapien	9 carci	σ.	Ŋ	P41495 sarcophaga	Ŋ	9 homos	P05486 conus geogr	37 conus	P83047 conus ventr		993 cyprinus c	P29177 bos taurus
SUMMARIES	ID	MACFI	FIBB ERYPA	FIBB PAPAN	FIBB PAPHA	FIBB_THEGE	ULAK MOUSE	CCAP_CARMA	TAL3_PICJA	IGAO_DACDE	TRM3_ECOLI	PLP_BRANA		UF03 MOUSE	UPA1_HUMAN	SAP STOVA	TAL1 PICJA		FAR1 ASCSU		RT33_BOVIN	UPA7 HUMAN	t i	FAR4_CALVO	OXYT_BUFRE	TMOF_SARBU	COW2_CONPU	GLUR_HUMAN		CONO_CONST		DNF1_LOCMI	ISOT_CYPCA	MGMT_BOVIN
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FESULT 2	FIBB_ERYPA	STANDARD;	PRT;	9 AA.
AC	P19346;	PRT	9 AA.	
DT	01-NOV-1990	Rel. 16,	Created	
DT	01-NOV 1990	Rel. 16,	Last sequence update	
DT	10-OCT-2003	Rel. 42,	Last annotation update	

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3 NEESL

P42996 scyliorhinu P4299 squalus aca P4299 scyliorhinu P23879 cyprinus ca P42998 eisenia foe P42998 eisenia foe P42994 raja clavat P43000 squalus aca P3840 ms musculu P81355 clostridium P25154 oryctolagus
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FIBB_THEGE
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FIBB PAPHA
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"Fibrinospetides A and B of baboons (Papio anubis, Papio hamadryas, and Theropithecus gelada: their amino acid sequences and evolutionary rates and a molecular phylogeny for the baboons.";
J. Biochem. 94:1973-1978 (1983).
-!- FUNCTION: Fibrinogen has a double function: yielding monomers that polymerize into fibrin and acting as a cofactor in platelet
                                                                                                                                                                                                                                                                                                                             guenons, and baboons.";
J. Biochem. 97:1487-1492(1985).
-!- FUNCTION: Fibrinogen has a double function: yielding monomers that polymerize into fibrin and acting as a cofactor in platelet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SUBJUTT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
(ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
-!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin, which cleaves fibrinopeptides A and B from alpha and beta chains, and thus exposes the N-terminal polymerization sites responsible for the formation of the soft clot.
                                                                                                                                                                                                                                                                                                                                                                                                                                           -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
(ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
-1- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin, which cleaves fibrinopeptides A and B from alpha and beta chains, and thus exposes the N-terminal polymerization sites responsible for the formation of the soft clot.
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Catarrhini, Cercopithecidae,
                                                                    Euteleostomi;
                                                                                                                                                                                                                                   Nakamura S., Takenaka O., Takahashi K., "Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and patas monkey (Erythrocebus aptas): their amino acid sequences, restricted mutations, and a molecular phylogeny for macaques,
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01-NOV-1990 (Rel. 16, Last sequence update)
10-CT-2003 (Rel. 42, Last annotation update)
Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment)
                                         Erythrocebus patas (Red guenon) (Hussar).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 18; DB 1; Length 9; Pred. No. 1.4e+05; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 AA; 1020 MW; 69FE7879C732CB1B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; D24180; D24180.
InterPro; IPR002181; Fibrinogen C.
PROSITE; PS00514; FIREN AG C DOMAIN; PARTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FIBRINOPEPTIDE B.
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Mammalia; Eutheria; Primates;
                                                                                                                     Cercopithecinae; Erythrocebus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32.7%;
80.0%;
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NCBI_TaxID=9555;
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"Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas,
"Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas,
"Fibrinopeptides A and B of baboons (Papio acid sequences and
evolutionary rates and a molecular phylogeny for the baboons.";
J. Biochem. 94:1973-1978 (1983).
-!- FUNCTION: Fibrinogen has a double function; yielding monomers that
polymerize into fibrin and acting as a cofactor in platelet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!-SUBBRIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.-!-PTM: Conversion of fibrinogen to fibrin is triaggered by thrombin, which cleaves fibrinopetides A and B from alpha and beta chains, and thus exposes the N-terminal polymerization sites responsible for the formation of the soft clot.
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Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Papio.
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P19342;
01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
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                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                          Score 17; DB 1; Length 9;
Pred. No. 1.4e+05;
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InterPro; IPROG12181; Fibrinogen C.
PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.
Blood coagulation; Plasma.
PIR; D28854; D28854.
InterPro; IRROD2181; Fibrinogen_C.
PROSITE; PSO0514; FIBRIN_AG_C_DOMAIN; PARTIAL.
Blood coagulation; Plasma.
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60.0%;
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9 AA; 1076 MW;
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Best Local Similarity 60.0
Matches 3; Conservative
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Best Local Similarity
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Furuya K., Liao S., Reynolds S.E., Ota R.B., Hackett M., Schooley D.A.;
Schooley D.A.;
"Isolation and identification of a cardioactive peptide from Tenebrio molitor and Spodoptera eridania.";
Biol. Chem. Hoppe-Seyler 374:1065-1074(1993).
-!- FUNCTION: The effect of CCAP is both ino- and chronotropic.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Stored in pericardial organs and released into the hemolymph.
PIR; A26363; A26363.
PIR; S27233; S27233.
                                                                                                                                                                                                                                                                                                                                                                                    SPECIES=C.maenas; TISSUE=Pericardial organs;
Stangier J., Hilbich C., Beyreuther K., Keller R.;
"Unusual cardioactive peptide (CCAP) from pericardial organs of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=93050343; PubMed=1426284;
Cheung C.C., Loi P.K., Sylwester A.W., Lee T.D., Tublitz N.J.;
Cheung Structure of a cardioactive neuropeptide from the tobacco
hawknoth, Manduca sexta.";
FEBS Lett. 313:165-168(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Transaldolase III (EC 2.2.1.2) (Fragment).
Pichia jadinii (Yeast) (Candida utilis).
Eukaryota; Fungi; Ascomycota; Saccharomyceties;
                                                                                                                                                                                                                                          Spodoptera eridania (Southern armyworm).
Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27.3%; Score 15; DB 1; Length 9; 100.0%; Pred. No. 1.4e+05; Ative 0; Mismatches 0; Indels
                                                                                                                                                                                        (Tobacco hornworm),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 AA; 959 MW; C5A861A9CDD44EB9 CRC64;
                                                                                                                                                                              (Green crab)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPECIES=T.molitor, and S.eridania; TISSUE=Head;
MEDLINE=94176032; PubMed=8129851;
                                                                                                                                                                                                                                                                                                  Eubrachyura, Portunoidea, Portunidae, Carcinus.
NCBI_TaxID=6759, 7130, 7067, 37547;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  shore crab Carcinus maenas.";
Proc. Natl. Acad. Sci. U.S.A. 84:575-579(1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomycetales; Saccharomycetaceae; Pichia
                                                                                                             01-0CT-1994 (Rel. 30, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Cardioactive peptide (CCAP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 AA.
                                                   9 AA.
                                                                                                                                                                            Carcinus maenas (Common shore crab) (Gre
Manduca sexta (Tobacco hawkmoth) (Tobacc
Tenebrio molitor (Yellow mealworm), and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AMIDATION
                                                                                              01-OCT-1994 (Rel. 30, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neuropeptide; Amidation.
DISULFID 3 9
                                                       STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPECIES=M.sexta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CN
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                                                          CARMA
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SEQUENCE
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TAL3 PIC
P17441;
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE.
                                                                         P38556
               RESULT 7
CCAP_CARMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                         MEDLINE=84161822; PubMed=6423621;
Nakamura S., Takenaka O., Takahashi K.;
Nakamura S., Takenaka O., Takahashi K.;
Isbirinopeptides A and B of baboons (Papio anubis, Papio hamadryas, and Theropithecus gelada): their amino acid sequences and evolutionary rates and a molecular phylogeny for the baboons.";
J. Bicochem. 94:1973-1978(1983).
-!- FUNCTION: Fibrinogen has a double function: yielding monomers that polymerize into fibrin and acting as a cofactor in platelet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                             aggregation.

SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS. FTM: Conversion of fibrinogen to fibrin is triggered by thrombin, which cleaves fibrinopeptides A and B from alpha and beta chains, and thus exposes the N-terminal polymerization sites responsible for the formation of the soft clot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (AUG-1998) to Swiss-Prot.
-!- MISCELIANEOUS: On the 2D-gel the determined pI of this unknown protein is: 6.0, its Mw is: 12.5 kDa.
SWISS-2DPAGE; P99031; MOUSE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mus musuculus (mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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15-DEC-1998 (Rel. 37, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Unknown protein from 2D-page of liver tissue (Spot 2D-0014LD)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sanchez J.-C., Rouge V., Frutiger S., Hughes G.J., Yan J.X., Hoogland C., Appel R.D., Binz P.-A., Hochstrasser D.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 16; DB 1; Length 9; Pred. No. 1.4e+05; 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30.9%; Score 17; DB 1; Length 9; 60.0%; Pred. No. 1.4e+05; tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NON TER 9 9 SEQÜENCE 9 AA; 1106 MW; B1E842C3240B145A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 AA; 977 MW; DDFE7879C7287B06 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FIK; FZ683*; FZ683*; Fibrinogen C.
InterPro; IPR02181; Fibrinogen C.
SOGSITE; PS00514; FIBRIN AG C DOMAIN; PARTIAL.
Blood coagulation; Plasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FIBRINOPEPTIDE B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 AA.
Theropithecus gelada (Gelada baboon)
                                                   Cercopithecinae, Theropithecus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29.1%;
50.0%;
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Matches 3; Conservative
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Best Local Similarity
Matches 3; Conserv
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1 NQEGL 5
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ID ULAK MOUSE
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SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Murphy D.J.; "Composition and role of tapetal lipid bodies in the biogenesis of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pollen coat of Brassica napks.";
Planta 208:588-598 (1999).
-!- FUNCTION: May play a structural role in the elaioplast, a tapetum-specific plastidial lipid organelle.
-!- TISSUE SPECIFICITY: Tapetum of anthers.
                                                                                                                                                    MEDLINE=88227859; PubMed=2836369;
MEDLINE=88227859; PubMed=2836369;
Inamoto S., Yoshioka Y., Ohtsubo E.;
Inamoto S., Yoshioka Y., Ohtsubo E.;
Indentification and characterization of the products from the traj and tray genes of plasmid R100.";
J. Bacteriol. 170:2749-2757(1988).
I- FUNCTION: TRANSFER GENE PROTEIN. IS INVOLVED IN THE CONJUGATION PROCESS OF BACTERIAL CELLS FOR THE EXCHANGE OF PLASMID DNA.
I- SUBCELLULAR LOCATION: Cytoplasmic.
I- SIMILARITY: Belongs to the tram family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids II, Brassicales, Brassicaceae, Brassica.
NCBI_TaxID=3708;
                                                                               Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=CV. TOPAZ; TISSUB=Tapetum;
MEDLINE=99349136; PubMed=10420651;
Hernandez-Pinzon I., Ross J.H.E., Barnes K.A., Damant A.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 13; DB 1; Length 5;
Pred. No. 1.4e+05;
1: Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 13; DB 1; Length 8;
Pred. No. 1.4e+05;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE 5 AA; 634 MW; 6B1B1AA443500000 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1099 (Rel. 39, Last annotation update)
Plastidial lipid-associated protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M20941; -; NOT_ANNOTATED_CDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; A32014; A32014. -
Conjugation; Plasmid; DNA-binding.
                                                                                                    Enterobacteriaceae, Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23.6%;
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66.7%;
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Best Local Similarity 66,77
Conservative
    TraM protein (Fragment).
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Best Local Similarity 66.7
Matches 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brassica napus (Rape)
                                                          Plasmid IncFII R100.
                                                                                                                    NCBI_TaxID=562;
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Avigad G., Markus Z.;

Avigad G., Markus Z.;

"Identification of a peptide inhibitor of galactose oxidase from
Dactylium dendroides.";

Ped. Proc. 31:447-447(1972).

-!- FUNCTION: Binds one copper ion per molecule but does not bind the
galactose oxidase appenryme. It may inactivate the enzyme by
binding to its prosthetic copper group.

PIR, A01341; XEYDGD.

COPPET, Metalloenzyme inhibitor.

SEQUENCE 7 AA; 706 MW; 75BB01A456D87DB0 CRC64;
                                                              Tsolas O., Sun S.C.;
"Isolation of a peptide containing a histidinyl-cysteinyl sequence from the active center of transaldolase.";
Arch. Biochem. Biophys. 167:525-531(1975).
-!- FUNCTION: Transaldolase is important for the balance of metabolites in the pentose-phosphate pathway.
-!- CATALYTIC ACTIVITY: Sedoheptulose 7-phosphate + D-glyceraldehyde 3-phosphate = D-erythrose 4-phosphate + D-fructose 6-phosphate.
-!- SATHWAY: Pentose phosphate pathway; nonoxidative part.
-!- SIMILARITY: Belongs to the transaldolase family. Subfamily 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Dactylium dendroides (Cladobotryum dendroides).

Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypomyces.
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100.0%; Pred. No. 1.4e+05;
iive 0; Mismatches 0;
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Pred. No. 1.4e+05;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Rel. 06, Created)
(Rel. 06, Last sequence update)
'Pol. 30, Last annotation update)
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(Rel. 13, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                     InterPro; IPR001585; Transaldolase.
PROSTIE; PS00958; TRANSALDOLASE 2; PARTIAL.
PROSTIE; PS01054; TRANSALDOLASE 1; PARTIAL.
Transferase; Pentose shunt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                             MEDLINE=75145197; PubMed=1092268;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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01-JAN-1990
28-FEB-2003
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P06294;
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TRM3_ECOLI
ID TRM3_ECOLI
AC P13973;
                           SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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nes 2; Conserv
        7 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 spectrometry."; FEBS Lett. 294:1
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P300<u>8</u>7;
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UPA1_HUMAN
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SAP_STOVA
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Chondrichthyes,
Elasmobranchii, Galeomorphii, Galeoidea, Carcharhiniformes, Triakidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               component.";
J. Biol. Chem. 258.3889-3894(1983).

-! SUBUNIT: Homopentamer. Pentaxin (or pentraxin) have a discoid arrangement of 5 noncovalently bound subunits.

-! SUBCELLULAR LOCATION: Secreted.

-! DISEASE: SAP IS A PRECURSON OF AMYLOID COMPONENT P WHICH IS FOUND IN BASEMENT MEMBRANE AND ASSOCIATED WITH AMYLOID DEPOSITS.

-! SIMILARITY: Belongs to the pentaxin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Robey F.A., Tanaka T., Liu T.-Y., "Isolation and characterization of two major serum proteins from the dogfish, Mustelus canis, C-reactive protein and amyloid P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=9500907; PubMed=7523108;
MEDLINE=95009907; PubMed=7523108;
Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
"Separation and sequencing of familiar and novel murine proteins
using preparative two-dimensional gel electrophoresis.";
Electrophoresis 15:735-745(1994).
-!- MISCELLANEOUS: On the 2D-gel the determined pl of this unknown
protein is: 5.1, its MW is: 36 kDa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-0CT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
01-0CT-1994 (Rel. 30, Last sequence update)
15-MRA-2004 (Rel. 43, Last annotation update)
Unknown protein from 2D-page of fibroblasts (P36) (Fragment).
Mus musculus (Mouse).
Eukarycai Metazoa: Achordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 AA; 965 MW; D05B5735B3386769 CRC64;
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PIR, B20569; B20569.

INCEPTO; IPR001759; PENTAXIN.

PROSITE; PS00289; PENTAXIN; PARTIAL.

Lectin; Amyloid; Glycoprotein; Plasma; Pentaxin.
                                                                                                                                                                                                                        01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-RDP-2003 (Rel. 41, Last annotation update)
Serum amyloid P-component (SAP) (Fragment).
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MEDLINE=83160932; PubMed=6403520;
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Echinoidea; Buechinoidea; Diadematacea; Phymosomatoida; Stomechinidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yoshimo K.-I., Takao T., Shimonishi Y., Suzuki N.; "Decermination of the amino acid sequence of an intramolecular disulfide linkage-containing sperm-activating peptide by tandem mass
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Plaama protein map: an update by microsequencing.";
Electrophoresis 13:707-714(1992)
-!- MISCELIANBOOUS: On the 2D-gel the determined pI of this unknown protein is: 4.9, its MW is: 65 kDa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lett. 294:179-182(1991).
FUNCTION: Cause stimulation of sperm respiration and motility
through intracellular alkalinization, transient elevations of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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15-MAR-2004 (Rel. 43, Last annotation update)
Unknown protein from 2D-page of plasma (Spot 2) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali
Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
Hochstrasser D.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21.8%; Score 12; DB 1; Length 8; 50.0%; Pred. No. 1.4e+05; ive 2; Mismatches 0; Indels
   21.8%; Score 12; DB 1; Length 7; 50.0%; Pred. No. 1.4e+05; rive 2; Mismatches 0; Indels
Length 7;
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01-MAR-1992 (Rel. 21, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Stomopneutes variolaris (SAP).
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MEDLINE=92097763; PubMed=1756858;
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                                                                                                                                                                                                                                                                                                                                                                                         01-APR-1993 (Rel. 25, Created)
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CC cAMP, cGMP and calcium levels in sperm cells, and transient
CC activation and subsequent inactivation of the membrane form of
CC guanylate cyclase.

FT DISULEID
SQ SEQUENCE 9 AA; 1010 MW; C469B3387B076EB9 CRC64;

Ouery Match
Best Local Similarity 66.7%; Pred: No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CNE 4

Db 3 CPE 5

Search completed: September 5, 2004, 11:04:00
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Q81v87 homo sapien
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Q65sf6 homo sapien
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Match Length DB
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Perfect score:
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rattus no scherichi mus muscu conodelphi rattus no	Q8jj20 gallus gall Q9zez9 buchnera ap Q9byy5 homo sapien Q15895 homo sapien Q15890 homo sapien	ursus macrop tragel echino megapt		Q9bfb2 sorex arane Q9bfb5 erinaceus c Q9bfb6 myrmecophag Q9bfb8 condylura c Q9bf88 eguus cabal Q9bf95 rousettus l Q9bf99 hylobates c
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118 119 210	22 23 25 26 26	27 29 30 31	8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	0.0 4 4 4 4 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5

ALIGNMENTS

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PRT; 8 AA. eated) st sequence update) st sequence update) ansferase, long chain base subunit ariant 1) (Fragment). Craniata; Vertebrata; Buteleostomi; Catarrhini; Hominidae; Homo. activity; IEA. activity; IEA. socre 18; DB 4; Length 8; bred. No. 1e+06; Mismatches 0; Indels 0; Gaps	
n base (Butell e; Homo bases. bases.	
te) chain base ent). rata; Eute nidae; Hot databases C64; Length 8	(e)
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ated) t sequence) t sequence) t sequence) traniati 1) (F raniata; Ve atarrhini; 1) L/GenBank/D ctivity; IE 3682CBBEB04 ore 18; DB red. No. 1e Mismatches	B B) equenc
1 1 OBLUBY PRELIMINARY; PRT; 8 AA OBLUB7, 01-MAR-2003 (TrEMBLrel. 23, Last sequence up 01-JUN-2003 (TrEMBLrel. 24, Last annotation) DJ10-JUN-2003 (TrEMBLrel. 24, Last annotation) PSPILC21. Homo sapiens (Human) BURALYOTA; Metazoa; Chordata; Craniata; Ver' Mammalia; Eutheria; Primates; Catarrhini; H NCBI TaxiD=9606; [1] SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEMBL; ALG50320; CAD54807.1; Transferase. 1 NON TER Transferase activity; IEA OO: 0016740; F:transferase activity; IEA Transferase. 1 NON TER Transferase. 1 NON TER TY MAtch TY MAtch 10.004; Pred. No. 1e+ Ches 2; Conservative 0; Mismatches	PRT; Created) Last seq
1 1 2021/87 PRELIMINARY; 2021/87; 2021/87; 201-MAR-2003 (TERMELRE1. 23, La 01-MAR-2003 (TERMELRE1. 24, La 01-JUN-2003 (TERMELRE1. 24, La 010-JUN-2003 (TERMELRE1. 24, La 010-JUN-2003 (TERMELRE1. 24, La 010-JUN-2003 (TERMELRE1. 24, La 010-JUN-2003 (TERMELRE1. 24, La 0110-JUN-2003 (TERMELRE1. 24, La Homo sapiens (Human). REACUTER (Aminotransferase) NOBLI, ALOSO320; CAD54807.1; - EMBLI, ALOSO32	13,
PRELIMINARY; (TEMBLrel. 23,	4 4 (Tremblrel: (Tremblrel:
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SULT 1 1V87 QB1V87; QB1V87; QB1V87; Q1-MAR-20 01-MAR-20 01-UJW-20 01-01JW-20	LT 2 29SAY7 09SAY7; 01-MAY-01-
RESULTA OBIV87 ID 00 ID 00 DT	QY Db Db Q9SAY7 ID Q1 DT ODT OT

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Wydner K.S., Mohan Raj B.K., Sciorra L.J., Roginski R.S., "The Mouse orthologue of the human ionotropic glutamate receptor-like gene (GRINLIA) maps to mouse chromosome 9." Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
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Ha-Lee Y.M., Lee J., Pyun H., Kim Y., Sohn J., Cho Y.J., Kim "Sequence variation of Hepatitis B virus promoter regions in persistently infected patients.";
Arch. Virol. 146:279-292 (2001).
EMBL, AR276526; AAG299311; -.
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NCBI_TaxID=10407;
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01-UTN-2003 (TrEMBLrel. 24, Last sequence update)
01-UTN-2003 (TrEMBLrel. 25, Last annotation update)
Peroxisome proliferator-activated receptor alpha (Fragment)
PPARA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32.7%; Score 18; DB 11; Length 9; 60.0%; Pred. No. 1e+06;
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Pred. No. 1e+06;
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BMBL; AF462416; AAO15648.1; JOINED.
MGD; MGI:107282; Grinlla.
GO; GO:0004872; F:receptor activity; IEA.
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01-MAR-2001 (TrEMBLrel. 16,
01-DEC-2001 (TrEMBLrel. 19,
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             Mus musculus (Mouse)
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Best Local Similarity
Matches 3; Conserv
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nes 2; Conserv
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                                                                                        NCBI TaxID=10090;
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                                                 Dioscorea tokoro.
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Dioscoreales, Dioscoreaceae,
                                                                                                                                                                                                                          STRAIN=20279211; PubMed=10821191; MEDLINE=20279211; PubMed=10821191; MEDLINE=20279211; PubMed=10821191; Terauchi R., Kahl G., Tarauchi R., Kahl G., Terauchi R., Kahl G., Terauchi R., Kahl G., Terauchi R., Kahl G., Terauchi R., Kahl G., Genet E., Seissel-Se0(2000). Teragions of Pal and Pgi genes from yams (Dioscorea)."; Mol. Genet E., Seissel-Se0(2000). EMBL, Abol6716; Bahls2231.; -GO; GO:0016853; F:isomerase activity; IEA.
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Dopico B., Jimenez T., Labrador E.;
"CDNA clones expressed in etiolated Cicer arietinum epicotyls.";
Submitted (SEP-2000) to the EMBL, GenBank/DDBJ databases.
EMBL; AJ299069; CAC10216.1; -.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Glutamate receptor ionotropic N-methyl D-aspartate-like IA
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Pred. No. 1e+06;
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01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein (Fragment)
Cicer arietinum (Chickpea) (Garbanzo).
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100.0%; Pred. No. 100.0%; O; Mismatches
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                        Phosphoglucose isomerase (Fragment)
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NCBL_TaxID=64475;
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GRINL1A.
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Dhar K., Chancock R.M, Lai C.-J.;
"Nonviral oligonucleock at the 5' terminus of cytoplasmic influenza viral mRNA deduced from cloned complete genomic sequences.";
Cell 21:495-500(1980).
EMBL: M25045; AAA43202.1; -.
NON_TER
                                          MEDLINE-22630144; PubMed-12745064;
Chew C.H., Samian M.R., Najimudin N., Tengku Muhammad T.S.;
"Molecular characterisation of six alternatively spliced variants and
                                                                                                                                                                                                                                                            Gaps
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                                                                             novel promoter in human peroxisome proliferator-activated receptor
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01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Influenza virus type A (Udorn/72) hemagglutinin (Seg 4) cDNA, 3'
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Truncated voltage-gated sodium channel alpha subunit (Fragment).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Influenza A viruses.
NCBI_TaxID=197911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                     30.9%; Score 17; DB 4; Length 9; 60.0%; Pred. No. 1e+06; tive 1; Mismatches 1; Indels
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                                                                                                  Biophys. Res. Commun. 305:235-243(2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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BMBL, AY258327; AA089523.1; -.
EMBL, AY258329; AA089523.1; -.
EMBL, AY258329; AA089523.1; -.
EMBL, AY258330; AA089525.1; -.
EMBL, AY258331; AA089526.1; -.
GO, GO:0004872; F:receptor activity; IEA.
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Matches 3; Conservative
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           NCBI_TaxID=9606;
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01-OCT-2002
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042564;
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MEDIAIDE=97442476; PubMed=9295353;

Plummar N.W., McBurney M.W., Meisler M.H.;

Plummar N.W., McBurney M.W., Meisler M.H.;

Alternative splicing of the sodium channel SCN8A predicts a truncated two-domain protein in fetal brain and non-neuronal cells.";

J. Biol. Chem. 272:24068-24015(1997).

GO; GO:0005216; P:ion channel activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nicotiana tabacum (Common tobacco).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots; asterids;
lamiids; Solanales; Solanaceae; Nicotiana.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Actinopterygii, Neopterygii, Teleostei, Euteleostei, Neoteleostei, Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes; Tetradontoidea, Tetraodontidae, Takifugu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=cv. PETIT HAVANA; Black Nitchell G.P., Robertson D., Slabas A.R., Wojtaszek P., Bolwell G.P.; Robertson D., Slabas A.R., "Proteomic study of secondary cell wall proteins from transformed
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7 AA; 730 MW; 75B72EA2C73772A0 CRC64;
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GO; GO:0005618; C:cell wall; IEA.
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Similarity 75.0%;
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9 AA; 922 MW; 21E8644EB7340EB8 CRC64;
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                                                         Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
"dUTPase minus CAEV is attenuated for pathogenesis and accumulates G
to A substitutions.";
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
BMBL; U81439; AB660832.1; -.
I...
SEMBL; U81439; AB660832.1; -.
SEMBL; U81439; AB600832.1; -.
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Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
EMBL, U81442; AAB60838.1; -.
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Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
"dUTPase minus CAEV is attenuated for pathogenesis and accumulates (to A substitutions.";
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U81441; AAB60836.1; -.
NON TER
SEQUENCE 9 AA; 922 MW; 21E8644EB7340EB8 CRC64;
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Caprine arthritis encephalitis virus (CAEV).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
VCBI_TaxID=11660;
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(TrEMBLrel. 04, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
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(TrEMBLrel. 04, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
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Viruses, Retroid viruses, Retroviridae, Lentivirus.
NCBI_TaxID=11660;
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Viruses; Retroid viruses; Retroviridae; Lentivirus
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01-UUL-1997 (TrEMBLrel. 0
01-DEC-2001 (TrEMBLrel. 1
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Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;

"duffrase minus CAEV is attenuated for pathogenesis and accumulates G
to A substitutions.";

Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.

EMBL; U81443; AAB60840.1; -.
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Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
"durpase minus CAEV is attenuated for pathogenesis and accumulates
to A substitutions.";
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.

EMBL; U81440; AAB60835.1; -.
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TAT.
Caprine arthritis encephalitis virus (CAEV).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
VCBI_TaxID=11660;
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
VCBI_TaxID=11660;
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27.3%; Score 15; DB 15;
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Live 0; Mismatches 0
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(TrEMBLrel. 04, I
(TrEMBLrel. 19, I
                                                 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 100.
hes 2; Conservative
                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                    01-JUL-1997 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
Tat protein (Fragment).
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Search completed: September 5, 2004, 11:05:41 Job time : 32.6667 secs

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5.1.6
Compugen Ltd.
GenCore version (c) 1993 - 2004
         Copyright
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- protein search, using sw model OM protein

5, 2004, 10:56:37; Search time 37.3333 Seconds (without alignments) 68.114 Million cell updates/sec September Title: Perfect score: Run on:

US-09-761-636A-9 55 1 CCNEESLIC 9 Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

1586107 segs, 282547505 residues Searched:

231240 Total number of hits satisfying chosen parameters:

seg length: 0 seg length: 9 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2003as;* geneseqp2003bs;* geneseqp2004s:* A Geneseq 29Jan04:* geneseqp1980s:* geneseqp1990s:* geneseqp2002s:* geneseqp2000s:* geneseqp2001s:* 2440678 Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Aay47045 Immunogen Abr28618 Human can Abr29242 Human can Aar47420 DhGF-acti		Aaw09330 FIV princ Abg99560 Conus sp Aar73351 Human TSH	Aar73350 Human TSH Aay87160 Human sec Aay875040 Feline im Aae06137 Himan gen		Aaw60376 Tumour ho Aaw93702 Human bre Aay48648 Membrane
AAY47045 ABR28618 ABR29242 AAR47420	AAR47390 AAR47421 AAR47419	AAW09330 ABG99560 AAR73351	AAR73350 AAY87160 AAY57040 AAE06137	ABG33960 AAR55115 AAW09328	AAW60376 AAW93702 AAY48648
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2 5 8 8 8 6 7 2 8 8 8 9 7 2 8 8 8 8 9 7 2 8 9 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	2227	27 27 26	2 0 0 0 7 7 7 7 7 9 9 0	7 5 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	7 7 7 8 8
26 27 28 29	3000	ო ო ო ო 4 ო	3 3 3 4 6 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	0444 010	4 4 4 6 4 7

ALIGNMENTS

VEGF based bicyclic dimeric peptide #2. AAU04528 standard; protein; 9 AA. (first entry) 26-SEP-2001 AAU04528; RESULT 1 AAU04528

Human; VEGP; vascular endothelial growth factor; angiogenesis; neovascularisation; lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic.

Synthetic

/note= "A disulfide bond forms between residue 1 and residue 1 of an identical peptide to form a dimeric peptide, or between residue 1 and residue 17 of the sequence appearing as AAU04527 also forming a dimeric peptide" Location/Qualifiers Key Disulfide-bond

/note= "This bond cyclises the peptide" 6. Disulfide-bond

WO200152875-A1

26-JUL-2001.

18-JAN-2001; 2001WO-US001533.

18-JAN-2000; 2000US-0176293P. 16-MAY-2000; 2000US-0204590P.

(LUDW-) LUDWIG INST CANCER RES.

Cendron A; Stacker S, Achen MG, Hughes RA,

WPI; 2001-442248/47.

Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine residues.

Claim 59; Page 32; 102pp; English.

Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine

residues.

Cendron A;

Stacker S,

Hughes RA,

Achen MG,

(LUDW-) LUDWIG INST CANCER RES

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revolutes, and a cyclic period with angiogenesis, neovascularisation are used to interfere with angiogenesis, neovascularisation or lymphangiogenesis in a mammal with a condition characterised by angiogenesis, neovascularisation or lymphangiogenesis, neovascularisation or lymphangiogenesis.

The condition is diabetic retinopathy, psoriasis, arthropathy, hemangioma, vascularised malignant or benign tumour, post-recovery cerebrovascular accident, post-angiopalsy restenosis, head, heat or cold crauma, substance induced neovascularisation of the liver, excessive hormone-related angiogenic dysfunction, diabetes induced neovascular sequelae, or chronic liver infection. The peptides are also used to modulate vascular permeability in a mammal (the mammal has a condition characterised by fluid accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain. The peptides are used to image blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are used to interfere with at least one biological activity induced by VEGF. VEGF-C or -D and are also used in combination with an anti-inflammatory agent, to treat a stabetic recovery.
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                 The sequence represents a dimeric bicyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human VEGFD (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring betabeta carbon separation distances on opposite antiparallel strands of a peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "A disulfide bond forms between residue 1 and residue 17 of the sequence appearing as AAU04527, forming a dimeric peptide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 neovascularisation, lymphangiogenesis, psoriasis, tumour, diabetes induced neovascular sequelae; rheumatoid arthritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diabetic retinopathy; chronic inflammation; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 55; DB 4; L 100.0%; Pred. No. 1.4e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VEGF based bicyclic dimeric peptide #9.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-JAN-2000; 2000US-0176293P.
16-MAY-2000; 2000US-0204590P.
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Best Local Similarity
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The sequence represents a dimeric bicyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human CV Wiscap (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring betacter carbon separation distances on opposite antiparallel strands of a peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptides (comprising 2 linked monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior comparation or lymphangiogenesis.

CC cyclisation are used to interfere with angiogenesis.

CC condition is diabetic retinopathy, psoriasis, atthropathy, chemangioma, vascularised malignant or benign tumour, post-recovery cerebrovascular accident, post-angioplasty restenosis, head, heat or cold trauma, substance-induced neovascularisation of the liver, excessive hormone-related angiogenic dysfunction, diabetes induced neovascular sequelae, hypertension induced neovascular sequelae, or chronic liver infection. The peptides are also used to modulate vascular permeability accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain. The peptides are used to image blood vessels and lymphatic cor brain. The peptides are used to image blood vessels and lymphatic virtual transmulation with at least one biological activity induced by VEEF, VEGF-C or D and are also used in combination with an anti-inflammatory agent, to treat a condition with an anti-inflammatory agent, to treat a condition release to the manner of the condition with an anti-inflammatory agent, to treat a condition with an anti-inflammatory agent, to treat and the condition and accident and and accident and an accident with an anti-inflammatory agent, to treat and the condition with an anti-inflammatory agent, to treat and the condition and accident and accident and accident and accident and accident and accident and a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             neovascularisation, lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90.9%; Score 50; DB 4; 177.8%; Pred. No. 1.4e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VEGF based bicyclic dimeric peptide #10.
                                                                                                                                                                                                                                                                             Example 26; Page 49; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diabetic retinopathy
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Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 9 AA;
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growth factor; angiogenesis;

.8 /note= "This bond cyclises the peptide"

Location/Qualifiers

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AAU04525 standard; peptide; 8 AA.
                                                                                                                                                                                                                                              26-SEP-2001 (first entry)
                                                                                                                                                                                                   7; Conservative
                                                                                                                                                                                                             1 CCNEESLIC 9
                                                                                                                                                                                               Sest Local Similarity
                WO200152875-A1
                                                                                                                                                                                      Sequence 9 AA;
                      26-JUL-2001
                                                    Achen MG,
                                                                        from an er
residues.
                                                                                                                                                                                                                                       AAU04525;
                                                                                                                                                                                             Query Match
                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                          RESULT 4
AAU04525
ID AAU0
XX
AC AAU0
XX
DT 26-S
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neovascularisation, lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic.
                                                                        Human; VEGF; vascular endothelial
                            based monocyclic peptide 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-MAY-2000; 2000US-0204590P.
                                                                                                                                                                                                                                                                                                                                                                                                            18-JAN-2001; 2001WO-US001533.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-JAN-2000; 2000US-0176293P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hughes RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-442248/47.
                                                                                                                                                                                                                                                  Disulfide-bond
                                                                                                                                                                                                                                                                                                                      WO200152875-A1
                                                                                                                                                                                                                                                                                                                                                                  26-JUL-2001
                                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Achen MG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              residues.
                            VEGF
         characterised by angiogenesis, neconsection or lymphanogenesis.

Characterised by angiogenesis, neconsection or lymphanogenesis.

The condition is diabetic retinopathy, psoriasis, arthropathy,

Chemangioma, vascularised malignant or benign tumour, post-recovery

cerebrovascular accident, post-angioplasty restenosis, head, heat or cord

trauma, substance-induced neovascularisation of the liver, excessive

crebrovascular accident, post-angioplasty restenosis, head, heat or cord

trauma, substance-induced neovascularisation of the liver, excessive

cremelae related angiogenic dysfunction, diabetes induced neovascular

sequelae, hypertension induced neovascular permeability

in a mammal (the mammal has a condition characterised by fluid

accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,

or brain. The peptides are used to inage blood vessels and lymphatic

vasculature. The monomeric and bicyclic peptides are used to interfere

with at least one biological activity induced by VEGF. Or -D and

are also used in combination with an anti-inflammatory agent, to treat a

chronic inflammation, especially rheumatoid arthritis, psoriasis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence represents a dimeric bicyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human VEGFD (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring betabet carbon separation distances on opposite antiparallel strands of a peptide loop fragment from an exposed loop of a growth factor protein and cyclishing the peptide by oxidising the cysteine residues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with anglogenesis,
residue 17 of the sequence appearing as AAU04527, forming a dimeric peptide" 2. .9
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 49; DB 4; Length 9;
Pred. No. 1.4e+06;
                                                                 /note= "This bond cyclises the peptide"
                                                                                                                                                                                                                                                                                                                                                              Cendron A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 26; Page 49; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                Hughes RA, Stacker S,
                                                                                                                                                                                                                                                                                                               (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89.1%;
77.8%;
                                                                                                                                                                                                                                              18-JAN-2000; 2000US-0176293P.
                                                                                                                                                                                                 18-JAN-2001; 2001WO-US001533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diabetic retinopathy
                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-442248/47.
                                            Disulfide-bond
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Cendron A;

Stacker S,

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The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human CYGFPO (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring betabet acrbon separation distances on opposite antiparallel strands of a peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidiasing the cysteins residues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior cyclisation are used to interfere with angiogenesis, cycyclisation or lymphangiogenesis in a mammal with a condition characterised by angiogenesis, neckscularisation or lymphangiogenesis. The condition is diabetic retinopathy, psoriasis, arthropathy, hemangioma, vascularised malignant or benign tumour, post-recovery cerebrovascular accident, post-angioplasty restenosis, had, had or cold trauma, substance-induced neovascularisation of the liver, excessive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hormome related angiogenic dysfunction, diabetes induced necessitian bermome related angiogenic dysfunction, diabetes induced necessitian sequelae, hypertension induced necessical sequelae, or chronic liver infection. The peptides are also used to modulate vascular permeability in a mammal (the mammal has a condition characterised by fluid accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain. The peptides are used to image blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are used to interfere with at least one biological activity induced by VEGF, VEGF-C or -D and are also used in combination with an anti-inflammatory agent, to treat a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chronic inflammation, especially rheumatoid arthritis, psoriasis and diabetic retinopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                              Claim 49; Page 32; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 CNEESLIC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CNEESLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 8 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
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Gaps 0

0; Indels

2; Mismatches

Sun Sep

Sequence 8 AA;

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Example 25; Page 47; 102pp; English
       AAU04539 standard; peptide; 8 AA.
                                VEGF based monocyclic peptide 17.
                                                                                                                          (LUDW-) LUDWIG INST CANCER RES.
                                                                                                              18-JAN-2000; 2000US-0176293P.
                                                                                                      18-JAN-2001; 2001WO-US001533.
                        (first entry)
                                                                                                                                   Achen MG, Hughes RA,
                                                                                                                                           WPI; 2001-442248/47.
                                                                         Disulfide-bond
                                                                                     WO200152875-A1.
                        26-SEP-2001
                                                                                              26-JUL-2001
                                                             Synthetic
               AAU04539;
                                                                                                                                                                residues.
RESULT 5
   AAU04539
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diabetic retinopathy

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Score 43; DB 4; Length 8; Pred. No. 1.4e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cendron A;
                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 25; Page 47; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stacker S,
                                                                                                                                                                                                                                                               AAU04541 standard; peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                        VEGF based monocyclic peptide 19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (LUDW-) LUDWIG INST CANCER RES.
78.2%;
87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-JAN-2001; 2001WO-US001533.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-JAN-2000; 2000US-0176293P.
16-MAY-2000; 2000US-0204590P.
                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hughes RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-442248/47.
                                                                                              CNEESLIC 9
                                                                                                                                          æ
                   Best Local Similarity Matches 7; Conserv
                                                                                                                         CNEETLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200152875-A1
                                                                                                                                                                                                                                                                                                                                                           26-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-JUL-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Achen MG,
                                                                                                                                                                                                                                                                                                            AAU04541;
                                                                                                N
Query Match
                                                                                                                                                                                                                RESULT 6
                                                                                                                                                                                                                                    AAU04541
                                                                                                                                          8
                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human vEGFD (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring beta carbon separation distances on opposite antiparallel strands of a peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with angiogenesis.

Consecuence of a nangiogenesis in a mammal with a condition characterised by angiogenesis in evascularisation or lymphangiogenesis.

Consecuence of a nangiogenesis in a mammal with a condition characterised by angiogenesis in evascularisation or lymphangiogenesis.

Consecuence of a nangiogenesis in a mammal with a condition condition is diabetic retinopathy, psoriasis, arthropathy heat or cold trauma, substance-induced neovascularisation of the liver, excessive hormone-related angiogenic dysfunction, diabetes induced neovascular sequelae, hypertension induced neovascular sequelae, or chronic liver sequelae, hypertension induced neovascular sequelae, or chronic liver in a mammal (the mammal has a condition characterised by fluid accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain. The peptides are also used to modulate vascular permeability in a mammal the mammal activity induced by VEGF, VEGF, or b and are also used in combination with an anti-inflammatory agent, to treat a continual or inflammatory agent, to treat a continual or inflammation with an anti-inflammatory agent, to treat a continual or inflammatory agent, to trea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine
                                                                                                                                                                                                                                      Human; VEGF; vascular endothelial growth factor; angiogenesis;
                                                                                                                                                                                                                                                             neovascularisation; lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "This bond cyclises the peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cendron A;
                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stacker S,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine residues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or cold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence represents a monomeric monocyclic peptide of the invention,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cerebrovascular accident, post-angioplasty restenosis, head, heat or col
trauma, substance induced neovascularisation of the liver, excessive
hormone-related angiogenic dysfunction, diabetes induced neovascular
sequelae, hypertension induced neovascular sequelae, or chronic liver
infection. The peptides are also used to modulate vascular permeability
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      characterised by angiogenesis, neovascularisation or lymphangiogenesis. The condition is diabetic retinopathy, psoriasis, arthropathy, hemangioma, vascularised malignant or benign tumour, post-recovery
          Gaps
     ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; VEGF; vascular endothelial growth factor; angiogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        neovascularisation, lymphangiogenesis, psoriasis, tumour, diabetes induced neovascular sequelae, rheumatoid arthritis, diabetic retinopathy, chronic inflammation, cyclic.
0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .8
/note= "This bond cyclises the peptide"
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with a condition

neovascularisation or lymphangiogenesis in a mammal

The condition is diabetic retinopathy, psoriasis, arthropathy, heady angiogenesis, neovascularisation or lymphangiogenesis. The condition is diabetic retinopathy, psoriasis, arthropathy, hemangioma, vascularised malignant or benign tumour, post-recovery creebrovascular accident, post-angioplasty restenosis, head, head or cold trauma, substance-induced neovascularisation of the liver, excessive hormone-related angiogenic dysfunction, diabetes induced neovascular sequelae, hypertension induced neovascular sequelae, or chronic liver infection. The peptides are also used to modulate vascular permeability in a mammal (the mammal has a condition characterised by fluid or brain. The peptides are used to inage blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are used to image blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are used to interfere with at least one biological activity induced by WGGF, WGGF-C or -D and are also used in combination with an anti-inflammatory agent, to treat a difference of the period are biologically rheumatoid arthritis, psoriasis and

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diabetic retinopathy

Sequence 8 AA;

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Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine
in a mammal (the mammal has a condition characterised by fluid accoundation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain. The peptides are used to image blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are used to interfere with at least one biological activity induced by VEGF. VEGF-C or D and are also used in combination with an anti-inflammatory agent, to treat a chronic inflammation, especially rheumatoid arthritis, psoriasis and
                                                                                                                                                                            Gaps
                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                      Human; VEGF; vascular endothelial growth factor; angiogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                 neovascularisation, lymphangiogenesis, psoriasis, tumour, diabetes induced neovascular sequelae, rheumatoid arthritis, diabetic retinopathy, chronic inflammation, cyclic.
                                                                                                                                               Score 42; DB 4; Length 8; Pred. No. 1.4e+06; 2; Mismatches 0; Indels

    .8
/note= "This bond cyclises the peptide"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cendron A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stacker S,
                                                                                                                                                                                                                                                                                               AAU04538 standard; peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                            VEGF based monocyclic peptide 16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                             76.4%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-JAN-2000; 2000US-0176293P.
16-MAY-2000; 2000US-0204590P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-JAN-2001; 2001WO-US001533
                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                          6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hughes RA,
                                                                                           diabetic retinopathy
                                                                                                                                                                                                     σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-442248/47.
                                                                                                                                                             Local Similarity
                                                                                                                                                                                                     CNEESLIC
                                                                                                                                                                                                                    CNEESVVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disulfide-bond
                                                                                                                      Sequence 8 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200152875-A1
                                                                                                                                                                                                                                                                                                                                                   26-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Achen MG,
                                                                                                                                                                                                     N
                                                                                                                                                                                                                                                                                                                        AAU04538;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               residues.
                                                                                                                                                Query Match
                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                  RESULT 7
AAU04538
 8866666666666
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence represents a monomeric monocyclic peptide of the invention,
                          Gaps
                          ·.
                                                                                                                                                                                                                                       Human; VEGF; vascular endothelial growth factor; angiogenesis;
                                                                                                                                                                                                                                                   neovascularisation, lymphangiogenesis, psoriasis, tumour, diabetes induced neovascular sequelae, rheumatoid arthritis, diabetic retinopathy, chronic inflammation, cyclic.
                        Indels
Score 41; DB 4; Length 8; Pred. No. 1.4e+06; 2; Mismatches 0; Indels

    .8
/note= "This bond cyclises the peptide"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cendron A;
                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 25; Page 47; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ŝ
                                                                                                                                      AAU04540 standard; peptide; 8 AA
                                                                                                                                                                                                             VEGF based monocyclic peptide 18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stacker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (LUDW-) LUDWIG INST CANCER RES
 74.5%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-JAN-2000; 2000US-0176293P.
16-MAY-2000; 2000US-0204590P.
                                                                                                                                                                                                                                                                                                                                                                                                                             18-JAN-2001; 2001WO-US001533
                                                                                                                                                                                      (first entry)
                          6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hughes RA,
                                                6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-442248/47.
Query Match
Best Local Similarity
Matches 6; Conserv
                                                               CNDESLLC
                                                2 CNEESLIC
                                                                                                                                                                                                                                                                                                                                       Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                          WO200152875-A1
                                                                                                                                                                                      26-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                    26-JUL-2001
                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                              AAU04540;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Achen MG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         residues
                                                                                                            RESULT 8
                                                                                                                          AAU04540
                                                                       셤
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The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human VEGFD (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring beta-beta carbon separation distances on opposite antiparallel strands of a peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with angiogenesis,

Example 25; Page 47; 102pp; English.

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whose 3-dimensional structure is modelled on the expose loop of human VBGFD (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring beta-beta carbon separation distances on opposite antiparallel strands of a peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptides by oxidising the cysteine residues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human, vascular endothelial growth factor; VEGF.A, vasculogenesis; angiogenesis; blood vessel; cancer; proliferative retinopathy; psoriasis; age-related macular degeneration; rheumatoid arthritis; cardiovascular;
                                                                                                                                                                                                                                                                       or cold
                                                                                                                                                                                                      characterised by anglogenesis, neovascularisaminator in the condition is diabetic retinopathy, psoriasis, arthropathy, hemangloma, vascularised malignant or benign tumour, post-recovery cerebrovascular accident, post-angloplasty restenosis, head, heat or cold trauma, substance-induced neovascularisation of the liver, excessive hormone-related anglogenic dysfunction, diabetes induced neovascular sequelae, hypertension induced neovascular sequelae, hypertension induced neovascular sequelae, or chronic liver in a mammal (the mammal has a condition characterised by fluid accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain. The peptides are used to image blood vessels and lymphatic or brain. The peptides are used to image blood vessels and lymphatic wasculature. The monomeric and bicyclic peptides are used to interfere with at least one biological activity induced by VEGF. Cor-D and are also used in combination with an anti-inflammatory agent, to treat a
                                                                                                                                                                    to cyclisation are used to interfere with angiogenesis, necovascularisation or lymphangiogenesis in a mammal with a condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chronic inflammation, especially rheumatoid arthritis, psoriasis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 39; DB 4; Length 8; Pred. No. 1.4e+06; 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide A6 encoded by human VBGF-A forward primer A6-F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU08451 standard; peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (LUDW-) LUDWIG INST CANCER RES (LICN ) LICENTIA OY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-FEB-2000; 2000US-0185205P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-FEB-2001; 2001WO-US006113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jeltsch MM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  primer; mutant; mutein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diabetic retinopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-536640/59.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 CNEESLIC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |||:| ||
CNEDSFIC 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAS12807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200162942-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alitalo K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU08451;
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The present invention relates to polypeptides that bind cellular receptors for vascular endothelial growth factors (VEGFs), the polyhucleotides encoding them, and their use for identifying agents that modulate interactions between VEGFs and their receptors. VEGFs and their receptors play an important role in vasculogenesis, the development of receptors play an important role in vasculogenesis, the development of and angiogenesis, the process of forming new blood vessels from precexisting ones. Modulators of interactions between VEGF and its receptors may be used to treat dystunction of the endothelial cell regulatory system. Such disorders include cancers, abnormal angiogenesis, rheumatoid proliferative retinopathies, age-related macular degeneration, rheumatoid arthritis and psoriasis. The polypeptides of the invention exhibit unique receptor binding profiles compared to known naturally occurring VEGFs.

AAUU8446-AAU08454 represent the peptides Al-A9 which are encoded by human VEGFA forward primers used in the methods of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, vascular endothelial growth factor; VBGF-C; vasculogenesis; angiogenesis; blood vessel; cancer; proliferative retinopathy; psoriasis; age-related macular degeneration; rheumatoid arthritis; cardiovascular;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polypeptides that bind cellular receptors for vascular endothelial growth
Polypeptides that bind cellular receptors for vascular endothelial growth
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                                                                                                                                                                                                                                                                                                                                                                                                                                     63.6%; Score 35; DB 4; Length 8; 71.4%; Pred. No. 1.4e+06; ive 1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide C6 encoded by human VEGF-C forward primer C6-F.
                 factors, polynucleotides encoding them.
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                                                     Claim 9; Fig 7C; 261pp; English.
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18-MAY-2000; 2000US-0205331P.
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nes 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 8 AA;
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receptors for vascular endothelial growth factors (VEGFS), the polymucleotides encoding them, and their use for identifying agents that modulate interactions between VEGFs and their receptors play an important role in vasculogenesis, the development of the embryonic vasculature from early differentiating endothelial cells and angiogenesis, the process of forming new blood vessels from pre-existing ones. Modulators of interactions between VEGF and its receptors system. Such disorders include cancers, abnormal angiogenesis, proliferative retinopathies, age-related macular degeneration, rheumatoid arthritis and psoriasis. The polypeptides of the invention exhibit unique receptor binding profiles compared to known naturally occurring VEGFs.

VEGF-C forward primers used in the methods of the present invention

Sequence 8 AA;

Score 33; DB 4; Lengtn 0;
Pred. No. 1.4e+06; 0; Mismatches 60.08; 71.48; Query Match
Best Local Similarity 71.*
Best Local Si Conservative 1 CCNEESL CCNSEGL ठ g

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Gaps ;

ABR29819 standard; peptide; 9 AA. ABR29819;

19-MAY-2003 (first entry)

Human cancer-related protein 192P2G7 HLA peptide #1263.

Human; cytostatic; vaccine; cancer; immune response; HLA; human leukocyte antigen

Homo sapiens

WO200283921-A2

10-APR-2002; 2002WO-US011654. 24-OCT-2002.

10-APR-2001; 2001US-0282739P. 10-APR-2001; 2001US-0283112P. 25-APR-2001; 2001US-0286630P.

(AGEN-) AGENSYS INC

Hubert RS; Ge ₩ Challita-Eid PM, Faris M, Morrison RK, Raitano AB; Jakobovits A, Morrison K,

WPI; 2003-075555/07

New composition comprising a substance that modulates the structure of proteins and polynucleotides, useful for therapeutic, prognostic and diagnostic reagents for eliciting cellular or humoral immune response in cancer patients.

Claim 13; Page 431; 1021pp; English.

The present invention relates to novel human cancer-related genes and proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and proteins are useful for eliciting a humoral or cellular immune response. The genes are useful as probes and primers for the amplification and/or detection of genes, mRNAs or their fragments, as reagents for the diagnosis and/or reproposis of cancer, as coding sequences capable of directing the expression of the protein, as tools for modulating or inhibiting the expression of genes and/or translation of transcripts, and RESULT 11
ABR29819
IAABR29819
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Gaps

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60.0%; Score 33; DB 6; Length 9; 71.4%; Pred. No. 1.4e+06;

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Query Match Best Local Similarity Matches 5; Conservat

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as therapeutic agents. The proteins and peptides are useful as therapeutic, prognostic and diagnostic reagents for cancer. The present sequence is a human leukocyte antigen (HLA) peptide, used in an example from the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                              vaccine; cancer; immune response; HLA;
                                                                                                                           Score 33; DB 6; Length 9; Pred. No. 1.4e+06; 1; Mismatches 1; Indels
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Morrison K, Morrison RK, Raitano AB;
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                                                                                                                                                                                                                                                                                                           ABR28797 standard; peptide; 9 AA.
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                                                                                                                         similarity 71.4%;
5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             human leukocyte antigen.
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Best Local Similarity
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ABR29456;

RESULT 13

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The present invention relates to novel human cancer-related genes and proteins (ABZ78120-ABZ78168 and ABR01861). The genes and proteins are useful for eliciting a humoral or cellular immune response. The genes are useful as probes and primers for the amplification and/or detection of genes, mRNAs or their fragments, as reagents for the diagnosis and/or prognosis of cancer, as coding sequences capable of directing the expression of the protein, as tools for modulating or inhibiting the expression of genes and/or translation of transcripts, as therapeutic genes. The proteins and peptides are useful as therapeutic, prognostic and diagnostic reagents for cancer. The present sequence is a human leukocyte antigen (HLA) peptide, used in an example from the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New composition comprising a substance that modulates the structure of proteins and polynucleotides, useful for therapeutic, prognostic and diagnostic reagents for eliciting cellular or humoral immune response in
                                                                                                                                                                                     Human, cytostatic, vaccine, cancer; immune response, HLA;
human leukocyte antigen.
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                                                                                                                        Human cancer-related protein 192P2G7 HLA peptide #258.
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71.4%; Pred. No. 1.4e+06;
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10-APR-2001; 2001US-0283112P
25-APR-2001; 2001US-0286630P
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ABR28814;
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Pred. No. 1.4e+06;
1; Mismatches 1; Indels
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10-APR-2001; 2001US-0283112P.
25-APR-2001; 2001US-0286630P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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                          CCNEESL 7
                                                                                          CCNAEAL 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
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Ge W

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Gaps

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1; Indels Length 9;

Homo sapiens

ABR28814 standard; peptide; 9 AA.

RESULT 14 ABR28814

Best Loc Matches

8 g

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10-APR-2001; 2001US-0282739P.
10-APR-2001; 2001US-0283112P.
25-APR-2001; 2001US-0286630P.
                 10-APR-2002; 2002WO-US011654.
                                       (AGEN-) AGENSYS INC.
   WO200283921-A2
          24-OCT-2002.
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Hubert RS; Ge ₩, Faris M, Jakobovits A, Challita-Eid PM, Faris Morrison K, Morrison RK, Raitano AB;

WPI; 2003-075555/07.

New composition comprising a substance that modulates the structure of proteins and polynucleotides, useful for therapeutic, prognostic and diagnostic reagents for eliciting cellular or humoral immune response in cancer patients.

Claim 13; Page 431; 1021pp; English.

The present invention relates to novel human cancer-related genes and proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and proteins are useful for eliciting a humoral or cellular immune response. The genes are useful as probes and primers for the amplification and/or detection of genes, mRNAs or their fragments, as reagents for the diagnosis and/or prognosis of cancer, as coding sequences capable of directing the expression of the protein, as tools for modulating or inhibiting the expression of genes and/or translation of transcripts, as therapeutic gents. The proteins and peptides are useful as sequence is a human leukocyte antigen (HLA) peptide, used in an example from the invention

Sequence 9 AA;

Gaps .; 0 60.0%; Score 33; DB 6; Length 9; 71.4%; Pred. No. 1.40+06; ive 1; Mismatches 1; Indels 5; Conservative Query Match Best Local Similarity Matches

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5, 2004, 11:03:33 Search completed: September Job time : 38.3333 secs

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; Sequence 33, Application US/09761636A
; Patent No. US20020065218A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
9, Conserve
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RESULT 2
US-09-761-636A-33
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US-09-761-636A-9
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Sequence 33, Appl
Sequence 34, Appl
Sequence 20, Appli
Sequence 22, Appl
Sequence 21, Appl
Sequence 11, Appl
Sequence 13, Appl
Sequence 142, Appl
Sequence 605, Appl
Sequence 222, Appl
Sequence 199, Appl
                                                                                 September 5, 2004, 11:05:54; Search time 35.6667 Seconds (without alignments) 79.502 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
                                                                                                                                                                                                                                                                                                                                                                           | Cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/US00_PUBCOMB.ppp:*
          GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-761-636A-34

US-09-761-636A-24

US-09-761-636A-20

US-09-761-636A-21

US-09-761-636A-19

US-09-761-636A-19

US-09-761-636A-19

US-09-761-636A-19

US-09-75-006A-193

US-09-75-006A-193

US-09-75-006A-193

US-09-784-211-199

US-09-84-271-199

US-09-84-271-199

US-09-138-2497
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                                                                                                                                                                                                                            1298764 seqs, 315065143 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                    Published_Applications_AA:*
                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                          OM protein - protein search, using sw model
                                                                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
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55
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Match Length
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900.9
899.1
783.6
746.2
746.4
700.9
700.9
600.0
600.0
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                                                                                     on:
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Sequence 93, Appl Sequence 93, Appl Sequence 109, Appl Sequence 109, Appl Sequence 106, Appl Sequence 106, Appl Sequence 93, Appl Sequence 115, Appl Sequence 108, Appl Sequence 115, Appl Sequence 13, Appl Sequence 13, Appl Sequence 16, Appl Sequence 116, Appl Sequence 116,
Sequence 2515, Ap
Sequence 2497, Ap
Sequence 2515, Ap
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Sequence 917, App
                                                                                                                                US-09-765-086-93
US-10-264-374-93
US-10-266-457-109
US-10-149-138-2516
US-10-149-138-3064
US-10-149-138-3064
US-10-149-138-3064
US-10-149-138-4059
US-10-149-138-4059
US-10-149-138-4029
US-10-149-138-4156
US-10-149-138-4156
US-10-149-138-4156
US-10-149-138-4156
US-10-149-138-4156
US-10-12-806A-13
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ALIGNMENTS

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Gaps
                                                                       APPLICANT: ACHEN, Marc
APPLICANT: ACHEN, Marc
APPLICANT: STACKER, Steven
APPLICANT: STACKER, Steven
APPLICANT: STACKER, Steven
TITLE OF INVENTION: VEGF-D/VEGF PEPTIDOMIMETIC INHIBITOR
FILE REFERENCE: 1064/48505 Achen et al
CURRENT APPLICATION NUMBER: US/09/761,636A
PRIOR APPLICATION NUMBER: US 60/176,293 .
PRIOR APPLICATION NUMBER: US 60/204,590
PRIOR PILING DATE: 2000-01-18
PRIOR PILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin version 3.0
SEQ ID NOS: 34
SEQ ID NOS: 34
SEQ ID NOS: 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 55; DB 9; Larity 100.0%; Pred. No. 1.2e+06; Conservative 0; Mismatches 0;
; Sequence 9, Application US/09761636A; Patent No. US20020065218A1; GENERAL INFORMATION:
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RESULT 5

US-09-761-636A-20

US-09-761-636A-20

Sequence 20, Application US/09761636A

Patent No. US20020065218A1

GENERAL INFORMATION:

APPLICANT: ACHEN, Marc

APPLICANT: STACKER, Steven

APPLICANT: CENDRON, Angela

TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR

FILE REFERENCE: 1064/48505 Achen et al

CURRENT APPLICATION NUMBER: US/09/761,636A

CURRENT FILING DATE: 2000-01-18

PRIOR APPLICATION NUMBER: US 60/176,293

PRIOR APPLICATION NUMBER: US 60/176,293

PRIOR APPLICATION NUMBER: US 60/204,590

PRIOR SEQ ID NOS: 34

SOFTWARE: Patentin Version 3.0

SEQ ID NO 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 22, Application US/09761636A

Patent No. US20020065218A1

GENERAL INFORMATION:
APPLICANT: ACHEN, Marc
APPLICANT: STACKER, Steven
APPLICANT: HUGHES, Richard
APPLICANT: GENDRON, Angela
TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
FILE REPERENCE: 1064/48505 Achen et al
CURRENT APPLICATION UNDERE: US/09/761,636A

CURRENT FILING DATE: 2001-01-18
VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                     Length 8;
                                                                                                                                                                                                                                                                                                                               83.6%; Score 46; DB 9; Le:
                FILE REFERENCE: 1064/48505 Achen et al CURRENT APPLICATION NUMBER: US/09/761,636A CURRENT FILING DATE: 2001-01-18
PRIOR APPLICATION NUMBER: US 60/176,293
PRIOR FILING DATE: 2000-01-18
PRIOR PILING DATE: 2000-05-16
PRIOR PILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin version 3.0
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87.5%;
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; ORGANISM: synthetic construct
US-09-761-636A-20
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Matches 7; Conservative
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Matches 8; Conservative
                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 CNEESLIC 9
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CNEETLIC 8
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US-09-761-636A-22
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            APPLICANT: ACHEM, Marc

APPLICANT: STACKER, Steven
APPLICANT: STACKER, Steven
APPLICANT: STACKER, Steven
APPLICANT: CENDRON, Angela
TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
FILE REFERENCE: 1064/48505 Achen et al
CURRENT APPLICATION NUMBER: US/09/761,636A
CURRENT FILING DATE: 2001-01-18
PRIOR FILING DATE: 2000-01-18
PRIOR FILING DATE: 2000-01-16
PRIOR APPLICATION NUMBER: US 60/204,590
PRIOR FILING DATE: 2000-01-16
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PATENTIN VERSION 3.0
SOFTWARE: PATENTIN VERSION 3.0
SOFTWARE: DATENTIN VERSION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: ACHEN, Marc
APPLICANT: ACHEN, Marc
APPLICANT: ACHEN, Steven
APPLICANT: HUGHES, Richard
APPLICANT: CENDRON, Angela
TITLE OF INVENITON: VEGF-J/VEGF PEPTIDOMIMETIC INHIBITOR
FILE REFERENCE: 1064/48505 Achen et al
CURRENT APPLICATION NUMBER: US/09/761,636A
CURRENT FILING DATE: 2001-01-18
PRIOR PPLICATION NUMBER: US 60/176,293
PRIOR PLING DATE: 2000-01-18
PRIOR PLING DATE: 2000-01-18
PRIOR PLING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PATENTIN VESTON 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89.1%; Score 49; DB 9; Length 9; 77.8%; Pred. No. 1.2e+06; tive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 34, Application US/09761636A Patent No. US20020065218A1
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Patent No. US202000665218A1
BERNEAL INFORMATION:
APPLICANT: ACHEN, Marc
APPLICANT: STACKER, Steven
APPLICANT: HUGHES, Richard
APPLICANT: CENDRON, Angela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: synthetic construct
US-09-761-636A-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) ORGANISM: Bynthetic construct US-09-761-636A-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 89.1
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CCNDESLLC 9
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Gaps

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PRIOR APPLICATION NUMBER: US 60/176,293

RESULT 4

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Gaps

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GENERAL INFORMATION: ANTERIALS AND METHODS INVOLVING HYBRID VASCULAR TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR TITLE OF INVENTION: ENDOTHELIAL GROWTH FACTOR DNAS AND PROTEINS TILE OF INVENTION: ENDOTHELIAL GROWTH FACTOR DNAS AND PROTEINS FILE REFERENCE: 28967/359778

CURRENT APPLICATION NUMBER: US 60/205,331

PRIOR APPLICATION NUMBER: US 60/205,331

PRIOR PRILING DATE: 2000-05-18

PRIOR PRILING DATE: 2000-05-25

NUMBER OF SEQ ID NOS: 175

SOFTWARE PATENTIN VET. 2.0

SOFTWARE PATENTIN VET. 2.0

SEQ ID NO 133

LENGTH: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 142, Application US/09795006A
Fatent No. US2020151680A1
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR
TITLE OF INVENTION: EMDOTHELIAL GROWTH FACTOR DNAS AND PROTEINS
TITLE OF INVENTION: EMDOTHELIAL GROWTH FACTOR DNAS AND PROTEINS
CURRENT APPLICATION NUMBER: US/09/795,006A
PRIOR PPLICATION NUMBER: US 60/205,331
PRIOR PPLICATION NUMBER: US 60/205,331
PRIOR FILING DATE: 2000-05-18
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 175
SOFTWARE: Patentin Ver. 2.0
SSEQ ID NO 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Description of Artificial Sequence: synthetic; OTHER INFORMATION: peptide
US-09-795-006A-133
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                                                                                                                                      Score 39; DB 9; Length 8; Pred. No. 1.2e+06; 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63.6%; Score 35; DB 9; Length 8; 71.4%; Pred. No. 1.2e+06; tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                Sequence 133, Application US/09795006A Patent No. US20020151680A1
      ; SEQ ID NO 21
; LENGTH: 8
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-21
                                                                                                                                        70.9%;
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ORGANISM: Artificial Sequence
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Best Local Similarity 71.47
                                                                                                                                    Query Match 70.9
Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                           2 CNEESLIC 9
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US-09-795-006A-133
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Sequence 21, Application US/09761636A

Patent No. US20020065218A1

GENERAL INFORMATION:

APPLICANT: ACHEN, Marc

APPLICANT: STACKER, Steven

APPLICANT: GENDRON, Angela

TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR

FILE REFERENCE: 1064/48505 Achen et al

CURRENT APPLICATION NUMBER: US/09/761,636A

CURRENT APPLICATION NUMBER: US 60/176,293

PRIOR PILING DATE: 2000-01-18

PRIOR APPLICATION NUMBER: US 60/204,590

PRIOR FILING DATE: 2000-01-18

PRIOR PILING DATE: 2000-05-16

NUMBER OF SEQ ID NOS: 34

SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 19, Application US/09761636A

Patent No. US20020065218A1

GENERAL INFORMATION:

APPLICANT: ACHEN, Marc

APPLICANT: ACHEN, Marc

APPLICANT: HUGHES, Richard

APPLICANT: HUGHES, Richard

APPLICANT: CENDRON, Angela

TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR

FILE REFERENCE: 1064/48505 Achen et al

CURRENT APPLICATION NUMBER: US 60/1761,636A

PRIOR APPLICATION NUMBER: US 60/176,293

PRIOR PILING DATE: 2000-01-18

PRIOR PILING DATE: 2000-01-18

PRIOR FILING DATE: 2000-05-16

NUMBER OF EGO ID NOS: 34

SOFTWARE: Patentin version 3.0

SEQ ID NO 19

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Pred. No. 1.26+06;
...arrhes 0; Indels
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Pred. No. 1.2e+06;
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PRIOR FILING DATE: 2000-01-18
PRIOR PEDILON NUMBER: US 60/204,590
PRIOR FILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 34
SOFTWARE PatentIn version 3.0
LENGTH: 8
                                                                                                                                                                                                                                       76.48;
75.08;
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                                                                                                                                                 TYPE: PRT
CRGANISM: synthetic construct
US-09-761-636A-22
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; ORGANISM: synthetic construct
US-09-761-636A-19
                                                                                                                                                                                                                                                                                      6; Conservative
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Best Local Similarity
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DEMONSTRATION:
TYPE: PRICE
ORGANISM: Conus dalli
FERATURE:
NAME: N
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47.3%; Score 26; DB 10; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.2e+06;
Matches 3; Conservative 1; Mismatches 0; Indels
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Publication No. US20030040088A1
GENERAL INFORMATION:
JAPPLICANT: Rosen et al.
TITLE OF INVENTION: 71 Human Secreted Proteins
FILE REPERENCE: PS7030P1
CURRENT APPLICATION NUMBER: US/09/984,271
CURRENT PILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: 09/482,273
PRIOR APPLICATION NUMBER: PCT/US99/15849
PRIOR APPLICATION NUMBER: 60/092,921
PRIOR FILING DATE: 1998-07-14
PRIOR FILING DATE: 1998-07-15
                                                                              APPLICANT: Cruz, Lourdes J.
APPLICANT: Grilley, Michelle
APPLICANT: Grilley, Michelle
APPLICANT: Schoenfeld, Robert M.
APPLICANT: Sherty, Reshma
APPLICANT: Sherty, Reshma
APPLICANT: Sherty, Robert M.
TITLE OF INVENTION: Cone Snail Peptides
FILE REFERENCE: 2314-249
CURRENT APPLICATION UNMBER: US/10/072,602B
CURRENT FILING DATE: 2002-02-11
PRIOR APPLICATION NUMBER: US 60/267,408
PRIOR APPLICATION NUMBER: US 60/267,408
PRIOR APPLICATION NUMBER: US 60/267,408
NUMBER OF SEQ ID NOS: 638
NUMBER OF SEQ ID NOS: 638
NUMBER OF SEQ ID NOS: 638
Watkins, Maren
Garrett, James E.
Cruz, Lourdes J.
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US-09-984-271-199
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| Publication No. US20040033907A1
| GENERAL INFORMATION:
| APPLICANT: Lee Frank D. APPLICANT: Chem. D. APPLICANT: Chem. John W. M. Man. John W. M. M. M. John W. M. John W. M. John W. J
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                                                                                                                                     Score 33; DB 9; Length 8; Pred. No. 1.2e+06; 0; Mismatches 2; Indels
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; Publication No. US20030109670A1
; GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Oliversity Baldomero M.
; APPLICANT: Oliversity Michael
                                                                                                                                 Query Match
Best Local Similarity 71.4%;
Matches 5; Conservative
    ; OTHER INFORMATION: peptide US-09-795-006A-142
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Best Local Similarity 100.
Matches 4; Conservative
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US-10-072-602B-292
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APPLICANT: Fikes, John
APPLICANT: Sette, Alessandro
APPLICANT: Sette, Alessandro
APPLICANT: Sidmey, John
APPLICANT: Suthwood, Scott
APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Ceiis, Esteban
APPLICANT: Keogh, Elissa
TITLE OF INVENTION: HERZ/neu Using Peptide and Nucleic Acid Compositions
TITLE OF INVENTION: HERZ/neu Using Peptide and Nucleic Acid Compositions
TITLE OF INVENTION: HERZ/neu Using Peptide and Nucleic Acid Compositions
TITLE OF INVENTION: UNBER: US/10/149,138
TITLE OF INVENTION NUMBER: US/10/149,138
FRIOR APPLICATION NUMBER: PT/USO0/33591
PRIOR APPLICATION NUMBER: PT/USO0/33591
PRIOR FILING DATE: 2000-12-11
PRIOR FILING DATE: 1999-12-11
NUMBER OF SEQ ID NOS: 4641
SOFTWARE: Patentin version 3.1
LENGTH: 8
TUBER OF SECOND SE
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                                                                           Sequence 199, Application US/09984276
Publication No. UG20030017500A1
GENERAL INFORMATION
APPLICANT: Rosen et al.
TITLE OF INVENTION: 71 Human Secreted Proteins
FILB REPERBREE: POS3091
CURRENT APPLICATION NUMBER: US/09/984,276
CURRENT FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: 09/482,273
PRIOR APPLICATION NUMBER: 60/092,921
PRIOR APPLICATION NUMBER: 60/092,921
PRIOR APPLICATION NUMBER: 60/092,922
PRIOR FILING DATE: 1998-07-15
PRIOR PILING DATE: 1998-07-15
PRIOR FILING DATE: 1998-07-15
PRIOR FILING DATE: 1998-07-15
PRIOR FILING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 267
SEQ ID NOS: 267
SEQ ID NO 199
LENGTH: 8
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; ORGANISM: Homo sapiens
US-09-984-276-199
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Matches 3; Conserv
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US-10-149-138-2497
RESULT 14
US-09-984-276-199
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Gaps

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Query Match 47.3%; Score 26; DB 15; Length 8; Best Local Similarity 60.0%; Pred. No. 1.2e+06; Matches 3; Conservative 2; Mismatches 0; Indels

1 CCNEE 5

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||:|:
| CCHEQ 5
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Search completed: September 5, 2004, 11:15:59 Job time : 36.6667 secs

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CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              212-751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 CNEESLIC 9
                                                                                                                                                                                                                                                                                                                                                   Patent No. 6090388
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: NY
                                                                                                                                                                                                                                                                                                                           US-09-100-409A-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-100-409A-27
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Sequence 31, Appl
Sequence 31, Appl
Sequence 13, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 49, Appl
Sequence 49, Appl
Sequence 1205, Appl
Sequence 17, Appl
Sequence 26, Appl
Sequence 37, Appl
Sequence 37, Appl
Sequence 37, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                      5, 2004, 11:01:38; Search time 12 Seconds (without alignments) 38.719 Million cell updates/sec
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/cgn2 6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2 6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2 6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2 6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2 6/ptodata/2/iaa/pcTUS_COMB.pep:*
         GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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PCT-US93-05325-3
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US-09-089-878-3
US-09-482-273-199
US-09-139-802-93
US-09-139-802-93
US-09-139-802-93
US-09-139-802-93
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US-09-139-802-13
US-09-125-107-13
US-08-107-411-7
US-08-107-411-7
US-09-258-754-49
US-09-258-754-49
US-09-258-75-107-49
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US-09-258-75-107-49
US-09-108-606-25
US-09-708-606-26
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US-09-717-364A-32
US-09-708-606-11
US-09-187-859-917
                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                         389414 segs, 51625971 residues
                                                                                                                                                                                                                                                                                                                                                   Maximum Match 100%
Listing first 45 summaries
                                                              - protein search, using sw model
                                                                                                                                                                                                              Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                          Issued Patents AA:*
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                                                                                                                                           US-09-761-636A-9
55
                                                                                                                                                                   1 CCNEESLIC 9
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Match Length
                                                                                       September
                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0 Maximum DB seq length: 9
                                                                                                                                                                                                 BLOSUM62
                                                                                                                                                                                                 Scoring table:
                                                                                                                                                        Perfect score:
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                                                            OM protein
                                                                                                                                                                        Sequence:
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                                                                                       Run on:
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33, Appli
42, Appl
214, App
33, Appl
42, Appl
214, Appl
79, Appl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: PEPTIDE COMPOSITION FOR
TITLE OF INVENTION: PREVENTION AND TREATMENT OF HIV INFECTION AND
TITLE OF INVENTION: IMMUNE DISORDERS
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSE: MORGAN & FINNEGAN
STREET: 345 Park Avenue
                                                                                           Sequence
Sequence
Sequence
                                                                                                                                                                                                                                   Sequence
                         Sequence
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Sequence
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Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
US-09-839-542B-917
US-09-708-666-20
US-09-0-535-927
US-09-073-551-14
US-08-973-551-14
US-09-079-433-3
US-09-258-754-42
US-09-258-754-42
US-09-258-754-42
US-09-042-107-42
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US-09-042-107-42
US-09-042-107-42
US-09-042-107-214
US-09-042-107-214
US-09-042-107-214
US-08-160-604-80
US-09-314-268-61
US-09-314-268-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
SOFTWARE: #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,409A
                                                                                                                                                                                                                                                                                                                                                            ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 1151-4154
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 27, Application US/09100409A Patent No. 6090388
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NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; LOCATION: 4
; OTHER INFORMATION:
; OTHER INFORMATION:
PCT-US93-05325-30
                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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Best Local Similarity
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0
      Sequence 2, Application PC/TUS9305325
GENERAL INFORMATION:
APPLICANT: STR, INTERNATIONAL
TITLE OF INVENTION: PEPTIDES CORRESPONDING TO ACTIVE DOMAINS
TITLE OF INVENTION: OF PLATELET-DERIVED GROWTH FACTOR (PDGF)
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: SRI INTERNATIONAL ATTN: INTELLECTUAL PROPERTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: SRI, INTERNATIONAL
TITLE OF INVENTION: OF PLATELET-DERIVED GROWTH FACTOR (PDGF)
NUMBER OF SEQUENCES: 39
CORRESPENDENCE ADDRESSE: SRI INTERNATIONAL ATTN: INTELLECTUAL PROPERTY
ADDRESSEE: SRI INTERNATIONAL ATTN: INTELLECTUAL PROPERTY
ADDRESSEE: COUNSEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 27; DB 5; Length 8; Pred. No. 3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/05225
FILING DATE: 19930603
CLASSIFICATION DATA:
FILING DATE: 05-070-103
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/894,497
FILING DATE: 05-070-1992
ATTORNEY/AGENT INPORMATION:
NAME: CLARK, JANET P.
REGISTRATION NUMBER: 34,799
REGISTRATION NUMBER: 34,799
REGISTRATION NUMBER: 34,799
REGISTRATION INPORMATION:
TELEPHONE: (415) 859-2446
TELEFRAX: (415) 859-2446
TELEFRAX: (415) 859-246
TELEFRAX: (415) 859-1880
TELER FAX: (415) 859-1880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 30, Application PC/TUS9305325 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 333 Ravenswood Avenue CITY: Menlo Park STATE: California COUNTRY: USA ZIP: 94025 COUNTRY: READABLE FORM: MEDIUM TYBE: Floppy disk COMPUTER: IBM PC compatible
                                                                                                                                                                                                                    STREET: 333 Ravenswood Avenue
CITY: Menlo Park
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 66.7
Lac 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 8 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear;
; MOLECULE TYPE: peptide
PCT-US93-05325-2
                                                                                                                                                                                                                                                                                                         ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CCNEES 6
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PCT-US93-05325-2
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SOFTWARE. PETENTIN BY SYSTEM: PC-DCS/MS-DOS
SOFTWARE. PETENTIN RAISES #1.0, Version #1.25
SOFTWARE. PETENTIN DATA:
SPELICATION NUMBER: PC-VIOS31/05325
FILING DATE: J9930603
STATIONEY ACREA THROUGH THE STATION STATI
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GENERAL INFORMATION:
APPLICANT: Groat, Randall G.
APPLICANT: Groat, Thomas P.
APPLICANT: Groat, Thomas P.
APPLICANT: Groat, Thomas P.
APPLICANT: Wermer, Brion
ITILE OF INVENTION: DIAGNOSIS OF FELINE IMMUNODEFICIENCY VIRUS INFECTION
ITILE OF INVENTION: USING ENVIORE BOLYPEPTIDE MARKERS
FILE REFERENCE: 00088/111001
CURRENT APPLICATION NUMBER: US/09/089,878
CURRENT FILING DATE: 1998-06-03
EARLIER APPLICATION NUMBER: US 60/085,615
BARLIER PILING DATE: 1998-05-15
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 3
LENGTH: 8
                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                           2; Indels
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Query Match

47.3%; Score 26; DB 4; Length 8;
Best Local Similarity 75.0%; Pred. No. 3e+05;
Matches 3; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 26; DB 4; Length 8; Pred. No. 3e+05;
                             Score 27; DB 5;
Pred. No. 3e+05;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Rosen et al.
TITLE OF INVENTION: 71 Human Secreted Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/482,273
CURRENT FILING DATE: 2000-01-13
EARLIER APPLICATION NUMBER: PCT/US99/15849
EARLIER FILING DATE: 1999-07-14
EARLIER FILING DATE: 1999-07-14
EARLIER FILING DATE: 1998-07-15
SOFTWARE: PALCATION NUMBER: 60/092,956
EARLIER FILING DATE: 1998-07-15
SOFTWARE: PALCATION NOS: 267
SOFTWARE: PALCATION NOS: 267
SOFTWARE: PALCATION NOS: 267
SOFTWARE: PALCATION NOS: 267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 199, Application US/09482273 Patent No. 6534631
                                                                                                                                                                                                                                                                     Sequence 3, Application US/09089878
Patent No. 6458528
                             49.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 37.5%;
Matches 3; Conservative
                                                                         4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
                             Query Match
Best Local Similarity
                                                                                                                1 CCNEES 6
                                                                                                                                                              3 CCNTSS 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CNONOFFC
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                                                                                                                                                                                                                            RESULT 6
US-09-089-878-3
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                                                                       Matches
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bond to corresponding position of identical
sequence."
                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 32, Application PC/TUS9305325
GENERAL INFORMATION:
APPLICANT: SRI, INTERNATIONAL
TITLE OF INVENTION: PEPTIDES CORRESPONDING TO ACTIVE DOMAINS
TITLE OF INVENTION: OF PLATELET-DERIVED GROWTH FACTOR (PDGF)
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: SRI INTERNATIONAL ATTN: INTELLECTUAL PROPERTY
ADDRESSEE: COUNSEL
                                                                                                                                                                                                                                                                                                                                   Score 27; DB 5; Length 8; Pred. No. 3e+05;
                                                                                                                                                                                                                                                                                                                                                                               2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/05325
                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                REGISTRATION NUMBER: 34,799
REPERENCE/DOCKET NUMBER: PCT-2679
TELEPHONE: (415) 859-2446
TELEPAX: (415) 859-2446
TELEX: 334486
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 19930603
CLASSIFICATION: NUMBER: 19030603
CLASSIFICATION: PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/894,497
FILING DATE: 05-UN-1992
ATTORNEY/AGENT INFORMATION:
NAME: CLARK, JANET P.
REGISTRATION NUMBER: 34,799
REFERENCE/DOCKET NUMBER: PCT-2679
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 859-2446
THEREPAX: (415) 859-3880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 333 Ravenswood Avenue
CITY: Menlo Park
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (415) 859-3880
TELEX: 334466
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                 49.1%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: Disulfide-bond
                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 66.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 8 amino acids
TYPE: AMINO ACID
TYPE: AMINO ACID
CLARK, JANET P.
                                                                                                                                                                                                                                                            ; MOLECULE TYPE: peptide
PCT-US93-05325-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 3..4
OTHER INFORMATION: /
OTHER INFORMATION: F
                                                                                                                                                                                                                                                                                                                                                                                                                   1 CCNEES 6
                                                                                                                                                                                                                                       TOPOLOGY: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 CCNTSS 8
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PCT-US93-05325-32
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1 CCNEESLIC 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-659-786-93
                                                           US-09-042-107-13
                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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Matches
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                                                                                                US-09-288-754-13
; Sequence 13, Application US/09258754
; Patent No. 6174687
; GENERAL INFORMATION:
APPLICANT: Rucelahti, Erkki
APPLICANT: Rajotte, Daniel
; TITLE CF INVENTION: Methods of Identifying Lung Homing Molecules Using
; TITLE CF INVENTION: Methods of Identifying Lung Homing Molecules Using
; TITLE CF INVENTION: Methods of Identifying Lung Homing Molecules Using
; TITLE CF INVENTION: Methods of Identifying Lung Homing Molecules Using
; FILE REFERENCE: P-LJ 3443
; CURRENT APPLICATION NUMBER: US/09/258,754
; CURRENT FILING DATE: 1999-02-26
; EARLIER FILING DATE: 1999-03-13
; NUMBER OF SEQ ID NOS: 452
; SEQ ID NOS: 452
; SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 93, Application US/09139802
Patent No. 6180084
GENERAL INFORMATION:
APPLICANT: Rucelahti, Erkki
APPLICANT: Pasqualini, Renata
TITLE OF INVENTION: NGR Receptor and Methods of Identifying Tumor Homing
TITLE OF INVENTION: Molecules That Home to Angiogenic Vasculature Using
FILE REFERENCE: P-LJ 3203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-258-754-13
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Pred. No. 3e+05;
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Pred. No. 3e+05;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/139,802
CURRENT FILING DATE: 1998-08-25
EARLIER PILING DATE: 1997-09-10
EARLIER FILING DATE: 1997-09-10
EARLIER FILING DATE: 1997-09-10
EARLIER FILING DATE: 1996-09-10
NUMBER OF SEQ ID NOS: 226
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Best Local Similarity 44.4%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 3; Conserv
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| | | |:
1 CCNQ 4
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                                          APPLICANT: Ruoslahti, Erkki
APPLICANT: Ragualini, Renata
TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
FILE REPERENCE: P-LJ 2892
CURRENT APPLICATION NUMBER: US/09/042,107
CURRENT APPLICATION NUMBER: US/09/042,107
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTHER INFORMATION: Description of Artificial Sequence: Synthetic COTHER INFORMATION: Peptide US-09-659-786-93
                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-042-107-13
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Pred. No. 3e+05;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                 Length 9;
                                                                                                                                                                                                                                                                                                                 Score 26; DB 3;
Pred. No. 3e+05;
                                                                                                                                                                                                                                                                                                                                                 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 93, Application US/09659786; Patent No. 6491894; GENERAL INFORMATION:
; Sequence 13, Application US/09042107; Patent No. 6232287; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 93, Application US/08926914
                                                                                                                                                                                                                                                                                                                   47.3%;
                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 44.4
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                 Local Similarity 33.
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US-08-926-914-93
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Pred. No. 3e+05;
    4; Mismatches
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CLASSIFICATION: 435
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US/07/844,303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 100, Application US/08397633A
Patent No. 5773577
GENERAL INFORMATION:
APPLICANT: Cappello, Joseph
                                                                                                                                                                                      Sequence 7, Application US/08107411
Patent No. 5340726
                                                                                                                                                                                                                                                                                                                                                                                                  E: Merck & Co., Inc.
P>O> Box 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Parr, Richard S.
REGISTRATION NUMBER: 32,586
REFERENCE/DOCKET NUMBER: 184
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (908) 594-4958
TELEFAX: (908) 594-4720
TELEX: (138825
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 60.0
Matches 3; Conservative
3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide
                                       1 CCNEESLIC 9
                                                                                 1 CLAKENVVC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: N.J.
COUNTRY: USA
ZIP: 07065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ||:|:
4 CCDEK 8
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US-08-397-633A-100
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Matches
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Fatent No. 6610651
General No. 9610651
General No. 6610651
General Republication
TITLE OF INVENTION: Molecules that Home to Various Selected Organs or TITLE OF INVENTION: Molecules that Home to Various Selected Organs or TITLE OF INVENTION: Molecules that Home to Various Selected Organs or TITLE OF INVENTION TISSUES
GURRENT FILING DATE: 2000-11-22
FRIOR APPLICATION NUMBER: US/09/722,250D
FRIOR PELING DATE: 1998-03-13
NUMBER OF SEQ ID NOS: 437
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
        GENERAL INFORMATION:
APPLICANT: Ruoslahti, Erkki
APPLICANT: Raosqualini, Renata
TITLE OF INVENTION: Tumor Homing Molecules, Conjugates
TITLE OF INVENTION: Derived Therefrom, and Methods of Using Same
CORRESPONDENCES ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-722-250D-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
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                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/926,914
FLING DATE: 10-SEP-1997
FLING DATE: 10-SEP-1997
ATIONEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REPERBNCE/DOKET NUMBER: P-LJ 2725
FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ 1D NO:
TELECAMINICATION SEQ 1D NO:
SEQUENCE CHARACTERISTICS:
FENCTH: 9 amino acids
                                                                                                                                                   ADDRESSEE: Campbell & Flores
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 26; DB 4;
Pred. No. 3e+05;
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Best Local Similarity 44.4%;
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                             United States
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                                                                                                                                                                                                                         California
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3Y: both
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Best Local Similarity
                                                                                                                                                                                                 CITY: San Diego
STATE: Californi
                                                                                                                                                                                                                                        COUNTRY: UN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-722-250D-13
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Gaps
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                                                                                                                                                                                                                                                                        APPLICANT: Waxman, Lloyd
APPLICANT: Connolly, Thomas M.
APPLICANT: Connolly, Thomas M.
APPLICANT: Connolly, Thomas M.
TITLE OF INVENTION: COLLAGEN-STIMULATED PLATELET AGGREGATION
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Cappello, Joseph
TITLE OF INVENTION: PRODUCTS COMPRISING SUBSTRATESCAPABLE
TITLE OF INVENTION: OF BNZYMATIC CROSS-LINKING
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/107,411
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ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
COUNTRY: Galfernia
COUNTRY: USA
ZIP: A111-14 USA
ZIP: S4111-14 USA
ZIP: S4111-14 USA
COMPUTER READALE FORM:
MUSICH TYPE: Floppy disk
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MUSICH TYPE: Flopp
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GenCore version 5.1.6
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OM protein - protein search, using sw model

September 5, 2004, 11:00:28; Search time 11.667 Seconds (without alignments) 74.205 Million cell updates/sec Run on:

US-09-761-636A-10 50 1 CSVPLTSVC 9 Perfect score: Sequence: Title:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 segs, 96191526 residues Searched:

790 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 9 Minimum DB a

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

KIES	Description	205K expantigen					T-cell receptor be	receptor	major protein ant	l recepto	last growt			orf dowstream to	seminal vesicle pr		Na+/K+-exchanging	formylglycinamide	addrecan - bovine	hio	unidentified 6.5/	Ig heavy chain CRD	hypothetical colla	seed protein ws-5	alcohol dehydrogen	enamelin f - bovin	coat protein beta	kidney and bladder	endosperm protein	
SOLMANIES	ΩI	G33098	A60356	PT0247	A60521	165546	PH0932	PH0803	E60274	F41946	A42057	A35180	A60522	B41983	I52974	149421	S29881	A12016	S42620	S59622	PQ0701	PT0268	A35039	E61491	871919	S10783	S13636	G58502	33	A32039
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ф	Query Match	34.0	32.0	32.0	30.0	30.0	30.0	30.0	28.0	28.0	28.0	28.0	28.0	28.0	28.0	26.0	26.0	26.0	26.0	26.0	26.0	26.0	24.0	24.0	24.0	24.0	24.0		24.0	22.0
	Score	17	16	16	15	15	15	15	14	14	14	14	14	14	14	13	13	13	13	13	13	13	12	12	12	12	12	12	12	11
			7	3	4	ហ	9	7	ထ	σι	10	11	12	13		15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

schwannomin - mous	R-phycoerythrin al	dnaA protein - Pse	Ig heavy chain CRD	catch-relaxing pep	dihydrofolate_redu	DNA topoisomerase	Iq H chain V-D-J r	acylase - Kluyvera	endoglycosylcerami	nitrate reductase	lectin - potato (f	T-cell receptor be	qene Cftr protein	major postsynaptic	granulocyte-colony
154357	B22565	B34835	PT0280	ECMUCR	I48105	148086	PH1602	S19288	B39745	S68802	S21288	PT0530	157018	A42689	154017
2	2	9	9	7 2	7	7 2	7 2	8	8	8	8	8	8	8	8 4
22.0	22.0	22.0	22.0	22.0	22.0	22.0	22.0	22.0	22.0	22.0	22.0	22.0	22.0	22.0	22.0
11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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205K exoantigen - malaria parasite (Plasmodium falciparum) (fragments) C.Species: Plasmodium falciparum C.Species: Plasmodium falciparum C.Species: 24-Aug-1990 #sequence_revision 24-Aug-1990 #text_change 09-Jun-2000 C.Accession: G33098 R.Nichols, J.H.; Hager, L.P. Submitted to the Protein Sequence Database, May 1990 A.Reference number: A33098 A.A.Accession: G33098 A.A.A.Cession: preliminary A.Molecule type: protein A.Residues: 1-8 A.NIC>
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Best Local Similarity
Matches 4; Conserv
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G33098
205K exoantigen
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2 VPLXLV 7 q

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RESULT 2

118K stomach cancer antigen - human (fragment)

C;Species: Home sapients (man) tragment (;Species: Home sapients (man) tragment (;Species: Home sapients (man) (for the context of the contex

Gaps °, 32.0%; Score 16; DB 2; Length 9; 50.0%; Pred. No. 2.8e+05; Live 1; Mismatches 2; Indels Best Local Similarity 50.0 Matches 3; Conservative Query Match

; 0

3 VPLTSV 8 :|| | 1 IPLKPV 6 qq à

Ig heavy chain CRD3 region (clone 2-106A) - human (fragment) C;Species: Homo sapiens (man) C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

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Figoria D. S., Correston, F., Correston, D., M. M. S., Vandenbark, A.A.; Wilson, D.B.
S. K. Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A; Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergants. PHOB91: MUID:92078857; PMID:1836012
A; Reference number: PHOB91; MUID:92078857; PMID:1836012
A; Molecule type: MRNA
A; Molecule type: MRNA
A; Residues: 1-7 < GOL>
A; Residues: 1-7 < GOL>
A; Residues: T-cell receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T-cell receptor alpha chain (J2) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PH0803
R;Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A;Title: T cell receptor genes in a series of class I major histocompatibility complex-rallelic exclusion and antigen-specific repertoire.
A;Reference number: PH0746; MUID:92078846; PMID:1836010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 major protein antigen MPT63 - Mycobacterium tuberculosis (fragment)
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 30-Sep-1993
C;Accession: E60274
R;Nagai, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.
R;Nagai, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.
A;Tit.le: Isolation and partial characterization of major protein antigens in the culture A;Reference number: A60274; MUID:91099989; PMID:1898899
                                    T-cell receptor beta chain V-D-J region (Clone 3) - rat (Liaguette)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C;Accession: PH0932
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                                receptor beta chain V-D-J region (clone 3) - rat (fragment)
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50.0%; Pred. No. 2.8e+05;
sive 1; Mismatches 1;
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33.3%; Pred. No. 2.8e+05;
tive 2; Mismatches 2;
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A;Cross-references: EMBL:X60912
A;Experimental source: T lymphocyte
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Matches 2; Conservative
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A,Molecule type: protein
A,Residues: 1-5 <NAG>
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CAAGIT 6
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Ribonamusa, L.; Baanante, I.V.
Comp. Biochem. Physiol. B 95, 295-310, 1990
A;Title: Purification and characterization of glycogen phosphorylase B from skeletal mus A;Reference number: A60521; MUD: 90227907; PMID: 2109669
A;Accession: A60521
A;Accession: A60521
A;Residues: 1-5 < BON>
C;Superfamily: glucan phosphorylase
C;Keywords: glycosyltransferase; hexosyltransferase; phosphoprotein
F;3/Binding site: phosphate (Ser) (covalent) (by phosphorylase b kinase) #status experim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Enhancer-like sequences and thei
C;Accession: PT0247

Y:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991

A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and A;Reference number: PT0222; MUID:91108337; PMID:1899102

A;Refeasion: PT0247

A;Residues: 1-9 < YZMA

A;Residues: 1-9 < YZMA

A;Residues: 1-9 < YZMA

A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MHC H2-L antigen - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C;Accession: I65546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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3; Conservative C
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Best Local Similarity
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SAPIDS 7
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Sperm-activating peptide SAP-IV - sea urchin (Diadema setosum)
C;Species: Diadema setosum
C;Species: Diagram, Species: Diadema Setosum
C;Species: Diadema Species: Diadema Diadema Species: Diadema Species: Diadema Species: Diadema Species: Diadema Diadem
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C;Species: Rattus norvegicus (Norway at)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C;Accession: 152974
R;Teng, C.T.; Harris, S.E.
BNA 2, 105-111, 1983
A;Title: The seminal vesicle secretion IV gene: detection of S1 nuclease-sensitive sites A;Accession: 152974; MUID:83261204; PMID:6307619
A;Accession: 152974
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C;Species: Azotobacter vinelandii
C;Species: Azotobacter vinelandii
C;Species: Azotobacter vinelandii
C;Accession: B41983
R;Grossman, M.J.; Hinton, S.M.; Minak-Bernero, V.; Slaughter, C.; Stiefel, E.I.
Proc. Natl. Acad. Sci. U.S.A. 89, 2419-2423, 1992
A;Title: Unification of the ferritin family of proteins.
A;Reference number: A41983; MUID:92196129; PMID:1549605
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A;Cross-references: GB:M83692; NID:g142297; PIDN:AAA22122.1; PID:g142299
A;Note: sequence extracted from NCBI backbone (NCBIP:88442)
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Pred. No. 2.8e+05;
1; Mismatches 0; Indels
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Best Local Similarity 66.7%;
Matches 2; Conservative
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                                                                                                                                                        T-cell receptor gamma chain (1a.27) - mouse (fragment)
(Cispecies: Mus musculus (house mouse)
Cispecies: Mus musculus (house mouse)
Cibate: 0.3 Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
Ciscossion: F41346
R;Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.
Mol. Cell. Biol. 11, 5902-5909, 1991
A;Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma ge
A;Reference number: A41946; MUID:92049316; PMID:1658619
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A;Title: Differential splicing in the extracellular region of fibroblast growth factor A;Reference number: A42057; MUID:92107200; PMID:1309595
A;Accession: A42057
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Aug-1990 #sequence_revision 10-Aug-1990 #text_change 21-Mar-1996
C;Accession: A35180
R;Yoshihara, Y:; Ueda, H.; Fujii, N.; Shide, A.; Yajima, H.; Satoh, M.
J; Biol. Chem. 265, 5809-5815, 1990
A;Title: Purification of a novel type of calcium-activated neutral protease from rat hancession: A35180
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C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 07-May-1999
C;Accession: A42057
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C;Keywords: growth factor receptor
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Best Local Similarity 66.7
Matches 2; Conservative
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A,Molecule type: protein
A,Residues: 1-8 <YOS>
C,Keywords: hydrolase
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RESULT 15
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Idminim B1 - western wild mouse (fragment)
C;Species: Mus spretus (western wild mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C;Accession: 149421
R;KO, M.S.; Wang, X.; Horton, J.H.; Hagen, M.D.; Takahashi, N.; Maezaki, Y.; Nadeau, J.H.
Mamm. Genome 5, 349-355, 1994
A;Title: Genetic mapping of 40 cDNA clones on the mouse genome by PCR.
A;Reference number: 148934; MUID:94319082; PMID:8043949
A;Reference number: preliminary; translated from GB/EMBL/DDBJ
A;Rectus: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-6 <RES>
A;Cross-references: EMBL:U05736; NID:9497073; PIDN:AAB60477.1; PID:g642829
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Pred. No. 2.8e+05;
0; Mismatches 1; Indels
Query Match

28.0%; Score 14; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels
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Best Local Similarity 66.7%;
Matches 2; Conservative (
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Search completed: September 5, 2004, 11:06:22 Job time: 11.6667 secs

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                                                                                                                                                         5, 2004, 10:57:02; Search time 7 Seconds (without alignments) 66.947 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd.
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TYS1 LITRU
UPAA HUMAN
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Maximum Match 100%
Listing first 45 summaries
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Match Length
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P38556 carcinus ma P05486 conus geogr P05487 conus stria P16339 locusta mig P32879 cyptinus ca P42994 raja clavat P82691 periplaneta P17440 pichia jadi P82099 litoria rub P13736 mytilus edu P13737 mytilus edu P58803 conus imper			(EC 2.1.1.63) (6-0-	a; Euteleostomi; Pecora; Bovoidea;	the bovine O6-methylquanine-DWA	methyltransferase."; Nucleic Acids Res. 18:17-21(1990)!- FUNCTION: Repair of alkylated guanine in DNA by stoichiometrically transferring the alkyl group at the 0-6 position to a cysteine residue in the enzyme. This is a suicide reaction: the enzyme is	uanine) + uanine) + protein	ogt methyltransferase	(BY SIMILARITY).	gth 9; Indels 0; Gaps		
CARNA CONGE CONGE CONGE CONGE CYPCA RAJCL PERAM PICJA MYTED MYTED MYTED	ALIGNMENTS	9 AA.	P29177; 01-DEC-1992 (Rel. 24, Created) 01-DEC-1992 (Rel. 24, Last sequence update) 01-OCT-1996 (Rel. 34, Last annotation update) Methylated-DNAprotein-cysteine methyltransferase methylguanine-DNA methyltransferase) (Fragment).	ca; Vertebrat Ruminantia;	of the bovine O6-m	guanine in DNA by t the O-6 position a suicide reaction	ining 6-0-methylguanine) thout 6-0-methylguanine)	A AND IDUES.	GROUP ACCEPTOR 720476047	19; DB 1; Len. No. 1.4e+05; smatches 2;		8 AA. e undare)
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00000000000		ST	el. el. on A	(Bovine). Metazoa; utheria; vinae; Bo	12; 11,	Res Rep rep rb rb	P C C	014 4 4 4 5 11 S	100₹	imilarity ; Conserva		ST2 (Rel.
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		T 1 BOVIN MGMT_BOVIN	P29177; 01-DEC-1992 01-DEC-1992 01-OCT-1996 Methylated-Imethylguanir	aurus Yota; l ilia; Ei lae; Bo	SEQUENCE. TISSUE=Thymus; MEDLINE=90174912; PubMed=2308822; RYdberg B., Hall J., Karran P., "Active site amino acid semence."	methyltransferase."; Nucleic Acids Res. 1 -!- FUNCTION: Repair transferring the residue in the e	irreversibly inactivated. CATALYTIC ACTIVITY: DNA ( [protein] - L-cysteine = DN		SITE	atch cal S	3 VPLTSVC : ::  3 IPILTPC	T 2 CARMA ACT CARMA P80709; 01-OCT-1996
ж ж ж ж ж ж ж ж ж ж ж ж ж ж ж ж ж ж ж		RESULT 1 MGMT_BOVIN ID MGMT_	P29 01- 01- Met			met Nuc -!-		-!- Int PRO DNA	ACT SEQUI	Query M Best Lo Matches		FΥ
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Gaps

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Indels

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Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
"Peptides from the skin glands of the Australian buzzing tree frog
Litori electrica. Comparison with the skin peptides from Litoria
                                                                                                                                                                                                                                                                                                                Litoria rubella (Desert tree frog).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
Pelodryadinae; Litoria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cydia pomonella (Codling moth).
Eukaryota, Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Eukaryota, Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Fortera, Endopterygota; Lepidoptera; Glossata; Ditrysia;
Tortricoidea; Tortricidae; Olethreutinae; Cydia.
NCBI_TaxID=82600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley Davey M., East P.D., Thorpe A.;
"Lepidopteran peptides of the allatostatin superfamily.";
Peptides 18:1301-1309(1997).
-! SIMILARITY: Belongs to the allatostatin family.
Mouropeptide; Amidation.
MOD_RES 8

AMIDATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 13; DB 1; Length 6;
Pred. No. 1.4e+05;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24.0%; Score 12; DB 1; Length 8; 66.7%; Pred. No. 1.4e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 - 6 AMIDATION.
6 AA; 792 MW; 6683704772C9A000 CRC64;
1.4e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                         (Rel. 41, Last sequence update)
(Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 AA.
                                                                                                                                                                                                                6 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
                  Pred. No. 1.46
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Amphibian defense peptide; Amidation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Aust. J. Chem. 52:639-645(1999).
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Skin.
                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=98054539; PubMed=9392829;
                                                                                                                                                                                                                                                       (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   h 26.0%;
Similarity 66.7%;
2; Conservative 1
                    75.0%;
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Matches 2; Conservative
                                      3; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Skin secretion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                    Best Local Similarity
                                                                           4 PLTS 7
                                                                                                               PRTS 7
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                                                                                                                                                                                                                                                       28-FEB-2003
                                                                                                                                                                                                                                                                         28-FEB-2003
10-OCT-2003
                                                                                                                                                                                                                EI01 LITRU
P82096;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rubella.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                            in all eukaryotic cells.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN IS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                               in various types of cell motility and are ubiquitously expressed
                                                                                                                                                                                                                   "A transaldolase. An enzyme implicated in crab steroidogenesis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Azotobacter vinelandii.
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Azotobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
0
                                                                                                                                                                      Lachaise F., Somme G., Carpentier G., Granjeon E., Webster S.,
Baghdassarian D.;
                            Carcinus maenas (Common shore crab) (Green crab).
Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Pleccyemata; Brachyura;
Eubrachyura; Portunoidea; Portunidae; Carcinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-92196129; PubMed-1549605;
Grossman M.J., Hinton S.M., Minak-Bernero V., Slaughter C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 14; DB 1; Length 8; Pred. No. 1.4e+05; 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Unification of the ferritin family of proteins."; Proc. Natl. Acad. Sci. U.S.A. 89:2419-2423(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
947 MW; DF98B5A1B417776D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 AA; 976 MW; 1424005AB2CAAEB3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
16-077-2001 (Rel. 40, Last annotation update)
Hypothetical protein in bfr 3'region (Pragment).
                                                                                                                                                                                                                                                                                                                                                6.8, ITS MW IS: 46 kDa.
-1- SIMILARITY: Belongs to the actin family.
InterPro; IPR004000; Actin like.
PROSITE; PS00406; ACTINS 1; PARTIAL.
PROSITE; PS00432; ACTINS 2; PARTIAL.
PROSITE; PS0132; ACTINS 2; PARTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28.0%; Score 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M83692; AAA22122.1; -. PIR, B41983. Hypothetical protein. NON_TER 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28.0%;
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Best Local Similarity 40.03
Matches 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Structural protein.
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TISSUE=Eyestalk;
MEDLINE=2195277; PubMed=11959015;
Sithigorngul P., Pupuem J., Krungkasem C., Longyant S.,
Chaivieuthangkura P., Sithigorngul W., Petsom A.;
"Seven novel FMRFamide-like neuropeptide sequences from the eyestalk
"Seven novel FMRFamide-like neuropeptide sequences from the eyestalk
"Seven novel FMRFamide-like neuropeptide sequences from the eyestalk
Comp. Biochem. Physiol. 131B:325-337(2002).
-!- SUBCELLULAR LOCATION: Secreted.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Treponema hyodysenteriae (Serpulina hyodysenteriae).
Bacteria; Spirochaetes; Spirochaetales; Brachyspiraceae; Brachyspira.
NCBI_TaxID=159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Flagellar filament outer layer protein flaA2 (35 kDa sheath protein)
                                                                            28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FFB-2003 (Rel. 41, Last annotation update)
FMRFamide-like neuropeptide FLP5 (SMPSLRLRF-amide).
FMRFamide-like neuropeptide fLP5 (SMPSLRLRF-amide).
Eukaryota, Metazoa; Arthropoda; Crustacea; Malacostraca;
Eukaryota, Metazoa; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 12; DB 1; Length 9;
Pred. No. 1.4e+05;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          GO; GO:0007218; P:neuropeptide signaling pathway; TAS. Neuropeptide; Amidation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B60B07340735A766 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBCELLULAR LOCATION: Periplasmic flagellum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AMIDATION
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                                                                                                                                                                                                                                             SEQUENCE, AND MASS SPECTROMETRY.
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66.7%;
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Matches 2; Conservative
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UNSURE 2 2
                                                                                                                                                                                                Penaeidae; Penaeus.
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AC P80159;
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Electrophoresis 13:707-714(1992).
-!- MISCELLANBOUGS: On the 2D-gel the determined pI of this unknown
protein is: 4.9, its MW is: 65 kDa.
SWISS-2DPAGE; P30087; HUMAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                          15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Allergen Fus s 13596* (Fragment).
Pusarium solani (subsp. pisi) (Nectria haematococca).
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae, Hypocreales; Nectriaceae, Nectria.
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1-APR-1993 (Rel. 25, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Unknown protein from 2D-page of plasma (Spot 2) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IISSUE=Plasma;
MEDIUNE-33092937; PubMed=1459097;
Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali
Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
Hochstrasser D.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 8;
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Verma J., Gangal S.V.;
Submitted (JUL-1997) to Swiss-Prot.
                                                                                                                                                                                                                                                                                                                                                                                            8 8 AA; 898 MW; C372C441F5B69041 CRC64;
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Pred. No. 1.4e+05;
1; Mismatches 0;
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Pred. No. 1.4e+05;
1; Mismatches 0,
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llarity 66.7%;
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Best Local Similarity
Matches 2; Conserv
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es 2; Conser
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1 LPL 3
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3 VPL 5
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6 NVP
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P81010;
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P43000;
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OXYV SQUAC
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Blasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
Scyliorhinidae; Scyliorhinus.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
Scyliorhinidae; Scyliorhinus.
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MEDLINE=95062247; PubMed=7972045;
Manuvet J., Rouille Y., Chauveau C., Chauvet M.-T., Acher R.;
"Special evolution of neurohypophysial hormones in cartilaginous fishes: asvatocin and phasvatocin, two oxytocin-like peptides
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                                                                              24.0%; Score 12; DB 1; Length 9; 66.7%; Pred. No. 1.46+05; tive 1; Mismatches 0; Indels
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                               855A19C68B4772D1 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NCV-1995 (Rel. 32, Created)
01-NCV-1995 (Rel. 32, Last sequence update)
01-NCV-1995 (Rel. 32, Last annotation update)
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
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ses 2; Conservative
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AA; 1129 MW;
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MEDLINE=96059313; PubMed=7591488;

Chauvet J., Michel G., Ouedraogo Y., Chou J., Chait B.T., Acher R.;

Chauvet J., Michel G., Ouedraogo Y., Chou J., Chait B.T., Acher R.;

identified in a dryness-resistant African toad, Bufo regularis.";

Int. J. Pept. Protein Res. 45:482-487(1995).

-!- FUNCTION: Devoid of oxytocic activity.

-!- SUBCELLULAR LOCATION: Secreted.

-!- SIMILARITY: Belongs to the vasopressin/oxytocin family.

InterPro; IRP000981; Neurhyp_horm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seritocin ([Ser5,Ile8]-oxytocin).
Bufo regularis (Leopard toad).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Bufo.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Chondrichthyes,
Elasmobranchii, Squalea, Squaloidei, Squalidae, Squalus.
NCBI_TaxID=7797;
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isolated from the spotted dogfish (Scyliorhinus caniculus).", Proc. Natl. Acad. Sci. U.S.A. 91:10266-11270 (1994).
- Proc. Natl. Acad. Sci. U.S.A. 91:10266-11270 (1994).
- FUNCTION: DISPLAYS OXYTOCIC ACTIVITY ON RAT UTERUS.
- SIMILARITY: Belongs to the vasopressin/oxytocin family. Interpro; IRR000981; Neurhyp_horm.
Pfam: PF00220; hormone4; 1. PR00181; PR00264; NEUROHYPOPHYS_HORM; 1.
                                                                                                                                                                                                                                                                                                                             Score 12; DB 1; Length 9;
Pred. No. 1.4e+05;
                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
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                                                                                                                                                                                                                      1 6 AMIDATION.
9 9 AMIDATION.
9 AA; 1016 MW; 17EDD76EB44449DB CRC64;
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9 AA; 983 MW; 17FF476EA5A6D04B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00220; hormone4; 1. PROSITE; PS00264; NEUROHYPOPHYS_HORM; FALSE_NEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 12; DB 1; I Pred. No. 1.4e+05;
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Last annotation update)
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01-NOV-1995 (Rel. 32, Last seq
10-OCT-2003 (Rel. 42, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last seq
01-NOV-1995 (Rel. 32, Last ann
                                                                                                                                                                                                                                                                                                                                   24.0%;
66.7%;
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50.0%;
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DISULFID 1
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Indels

Pred. No. 1.4e+05; Mismatches 0;

100.08; Pr.

Conservative

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Matches

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Best Local Similarity

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                                                                              acner R., Chauvet J., Chauvet M.-T., "Phylogeny of the neurohypophysial hormones. Two new active peptides isolated from a cartilaginous fish, Squalus acanthias.";

Bur. J. Biochem. 29:12-19(1972).
                                                                                                                                                                                                                                                                                 MEDLINE-72128038; PubMed=4622083;
Acher R., Chauvet J., Chauvet M.-T., Fontaine M.;
Acher R., Chauvet J., Chauvet M.-T., Fontaine M.;
Identification of 2 new neurohypophyseal hormones, valitocin (Val8-oxytocin) and aspartocin (Asn4-oxytocin) in a selachian fish, the spiny dog-fish (Squalus acanthias).";
C. R. Acad. Sci., D., Sci. Nat. 274:313-316(1972).
C. R. Acad. Sci., D., Sci. Nat. 274:313-316(1972).
InterPro; IPR000981; Neurhyp_horm.
Pfam, PF00220; hormone4; 1.
HORNOSTES, PS00264; NORNOHYPENPYS_HORM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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-!- FUNCTION: COMPONENT OF THE BASAL LAYER IN WHICH THE CAPSIDS ARE EMBEDDED. BINDS DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Capsid assembly and DNA maturation protein (Virion protein UL38)
(Capsid protein VP19C) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Herpes simplex virus (type 1 / strain KOS).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Simplexvirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOD_RES 9 9 AMIDATION.
SEQUENCE 9 AA, 996 MW; 17EDD76EB456D04B CRC64;
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Pred. No. 1.4e+05;
0; Mismatches 1;
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                                                          MEDLINE=73031727; PubMed=5083097;
Acher R., Chauvet J., Chauvet M.-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=91101287; PubMed=1846198;
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66.7%;
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Best Local Similarity
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SEQUENCE.
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VP19 HSV1K
VP19 HSV1K
AC P232T0
DT 01-NOV
DT 0
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DB 1; Length 6;

22.0%; Score 11;

703 MW; 67376451A336F000 CRC64;

Capsid assembly; Coat protein; DNA-binding

NON TER SEQUENCE

Query Match

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                                                                                                                                                                                                                                                     -!- FUNCTION: This peptide exhibits both potentiating (contraction) and inhibitory (relaxation) effects on the anterior byssus
   01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
01-MAR-1989 (Rel. 10, Last sequence update)
Catch-relaxing peptide (CARP).
Catch-relaxing peptide (CARP).
Bukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloida; Mytiloides, Mytilidae; Mytiluse.
Mytiloidea; Mytilidae; Mytilus.
                                                                                                                                                                            MEDLINE=88052022; Pubmed=3676797;
Hirata T., Kubota I., Takabatake I., Kawahara A., Shimamoto N.,
Muneoka Y.;
                                                                                                                                                                                                                       "Catch-relaxing peptide isolated from Mytilus pedal ganglia.";
Brain Res. 422:374-376(1987).
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7 AA; 831 MW; 6734072687669DB0 CRC64;
 7 A.A.
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Best Local Similarity 25.00,
Local 1; Conservative
 STANDARD;
                                                                                                                                                                                                                                                                                  retractor muscle. A29342; ECMUCR.
                                                                                                                                                                                                                                                                                                                Hormone; Amidation.
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CARP MYTED
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SEQUENCE
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